

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:42:50 ; Search time 268.17 Seconds  
(without alignments)  
3418.847 Million cell updates/sec

Title: US-09-801-115-1  
Perfect score: 534  
Sequence: 1 gtcccaactcgaagtgaaag.....aaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:\*  
6: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:\*  
7: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1986.DAT:\*  
8: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:\*  
9: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:\*  
10: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1989.DAT:\*  
11: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1992.DAT:\*  
14: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:\*  
15: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1994.DAT:\*  
16: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1996.DAT:\*  
18: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1997.DAT:\*  
19: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1998.DAT:\*  
20: /SID5/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:\*  
21: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:\*  
22: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SID5/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 534   | 100.0       | 534    | AAA38006 | Uck-1 nucleotide s  |
| 2          | 507   | 94.9        | 655    | AA544932 | Human encoding nove |
| 3          | 498.2 | 93.3        | 538    | AAH98515 | Human EST-derived   |
| 4          | 498.2 | 93.3        | 538    | AAH98548 | Human EST-derived   |
| 5          | 497.2 | 93.1        | 558    | AAH34835 | Human colon cancer  |
| 6          | 493.4 | 92.4        | 515    | AAH87730 | Human secreted pro  |
| 7          | 493.4 | 92.4        | 515    | AAH64012 | CDNA encoding huma  |
| 8          | 486.6 | 91.1        | 506    | AAV59598 | Human secreted pro  |
| 9          | 478.6 | 89.6        | 506    | AAV59746 | Human secreted pro  |

|    |       |      |       |    |          |                    |
|----|-------|------|-------|----|----------|--------------------|
| 10 | 466.8 | 87.4 | 500   | 20 | AA97826  | Human secreted pro |
| 11 | 465.4 | 87.2 | 467   | 21 | AA15929  | Human protein clon |
| 12 | 411.4 | 77.0 | 413   | 20 | AA97873  | Human secreted pro |
| 13 | 405.4 | 75.9 | 415   | 21 | AAC00147 | Human secreted pro |
| 14 | 335   | 62.7 | 663   | 20 | AA234051 | Human PRO772 nucle |
| 15 | 335   | 62.7 | 663   | 21 | AACT8498 | Human PRO772 nucle |
| 16 | 335   | 62.7 | 663   | 21 | AAC58238 | CDNA encoding nove |
| 17 | 327.2 | 61.3 | 908   | 22 | AA544933 | Human secreted pro |
| 18 | 321.8 | 60.3 | 669   | 21 | AAH87771 | CDNA encoding huma |
| 19 | 321.8 | 60.3 | 669   | 22 | AAH64055 | Human secreted pro |
| 20 | 309.8 | 58.0 | 354   | 20 | AAH41509 | Human secreted pro |
| 21 | 309   | 57.9 | 637   | 21 | AAZ56747 | Human transmembran |
| 22 | 300   | 56.2 | 566   | 22 | AA545120 | CDNA encoding nove |
| 23 | 300   | 56.2 | 566   | 22 | AA545121 | CDNA encoding nove |
| 24 | 295.4 | 55.3 | 297   | 21 | AAH15919 | Human protein clon |
| 25 | 272   | 50.9 | 392   | 21 | AAH16090 | Human colon cancer |
| 26 | 224.4 | 42.0 | 459   | 21 | AAH38007 | Uck-2 nucleotide s |
| 27 | 214.4 | 40.1 | 6021  | 22 | AAH82407 | Human immune/haema |
| 28 | 214.4 | 40.1 | 13744 | 22 | AAH82406 | Human immune/haema |
| 29 | 214.4 | 40.1 | 13744 | 22 | AAH82405 | Human secreted pro |
| 30 | 214   | 39.4 | 269   | 21 | AAH97651 | Extended human sec |
| 31 | 210.2 | 39.4 | 321   | 20 | AAH97651 | Human EST DNA43509 |
| 32 | 185.2 | 34.7 | 495   | 20 | AAH97651 | CDNA encoding spr  |
| 33 | 185.2 | 34.7 | 495   | 21 | AAH97651 | Human immune/haema |
| 34 | 185.2 | 34.7 | 495   | 22 | AAH97651 | Human immune/haema |
| 35 | 184.8 | 34.6 | 2953  | 22 | AAH68359 | Human secreted exp |
| 36 | 184.8 | 34.6 | 2953  | 22 | AAH68360 | Human transmembran |
| 37 | 178.8 | 33.5 | 379   | 21 | AAH41312 | Human gene regulat |
| 38 | 160.8 | 30.1 | 465   | 22 | AAH41312 | Uck-4 nucleotide s |
| 39 | 158.4 | 29.7 | 6283  | 24 | AAH61352 | Uck-3 nucleotide s |
| 40 | 130.6 | 24.5 | 363   | 21 | AAH38009 | Human gene regulat |
| 41 | 127   | 23.8 | 204   | 21 | AAH38008 | Human EST-derived  |
| 42 | 119.4 | 22.4 | 6283  | 24 | AAH61351 | Human EST-derived  |
| 43 | 102.2 | 19.1 | 948   | 22 | AAH98012 | Human EST-derived  |
| 44 | 78.4  | 14.7 | 844   | 22 | AAH98802 | Human EST-derived  |
| 45 | 78.4  | 14.7 | 66566 | 21 | AAH53450 | Human thiredoxin   |

## ALIGNMENTS

RESULT 1  
ID AAA38006 standard; CDNA: 534 BP.  
XX AAA38006;  
AC  
XX 22-AUG-2000 (first entry)  
XX  
XX  
XX Uck-1 nucleotide sequence.  
DE  
XX  
XX Uck-1: chemotaxis factor; immunocyte; haemopoiesis stimulant; tumour;  
KW radiotherapy; chemotherapy; human; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
XX CN1244584-A.  
PN 16-FEB-2000.  
XX  
XX 14-MAY-1999; 99CN-0107284.  
XX  
XX 14-MAY-1999; 99CN-0107284.  
XX  
XX (UYBE-) UNIV BEIJING MEDICAL.  
XX  
XX Ma D, Han W, Zhang Y;  
XX  
XX WPI: 2000-388170/34.  
XX P-PSDB; AAH98142.  
XX  
XX Chemotactic factor useful for treatment and diagnosis of immunocyte  
XX disorders - has immunocyte chemotactic stimulating factor  
PT

XX Example 4; Fig 1; 31pp; chinese.  
PS  
XX

CC factor polypeptide. The UCR-1 cDNA sequence encoding a chemotaxis  
CC activity and a haemopoiesis stimulating effect. The invention relates to  
CC UCR proteins, their encoding nucleotide sequences and antibodies and  
CC antagonists against the proteins. The nucleotide and protein sequences  
CC are useful for the preparation of a composition for the diagnosis and  
CC treatment of diseases associated with abnormal immunocyte function and  
CC low haemopoiesis function caused by radiotherapy and chemotherapy used  
CC to treat tumours and other diseases.

sequence 534 BP; 156 A; 110 C; 134 G; 134 T; 0 other;

|                           |        |                     |        |             |
|---------------------------|--------|---------------------|--------|-------------|
| Query Match               | 100.0% | Score 534;          | DB 21; | Length 534; |
| Best Local Similarity     | 100.0% | Pred. No. 3.5e-107; |        |             |
| Matches 534; Conservative | 0;     | Mismatches          | 0;     | Indels 0;   |

|    |     |  |     |
|----|-----|--|-----|
| QY | 1   | gtccccaactctggaagtcgaagccgagctctggcgagaaagtgaaggagggcggtgctccgcg | 60  |
| Db | 1   | gtccccaactctggaagtcgaagccgagctctggcgagaaagtgaaggagggcggtgctccgcg | 60  |
| QY | 61  | cggttgccggttgctatcgcttcgcgaacaactctcaagcagccagcttagaagagttgag    | 120 |
| Db | 61  | cggttgccggttgctatcgcttcgcgaacaactctcaagcagccagcttagaagagttgag    | 120 |
| QY | 121 | ggaaagtcgtcgcgcgtgcgtgtctgcagacgcggttgatatactgtgcagccggaataaaca  | 180 |
| Db | 121 | ggaaagtcgtcgcgcgtgcgtgtctgcagacgcggttgatatactgtgcagccggaataaaca  | 180 |
| QY | 181 | tgcgccctctgcctccaagtgtgaaagcgccagctgaaaga tgcctgcgctcgatatacca   | 240 |
| Db | 181 | tgcgccctctgcctccaagtgtgaaagcgccagctgaaaga tgcctgcgctcgatatacca   | 240 |
| QY | 241 | ctcactgtgtaacaacagtatctatcatatgctatctgtgttgccactgataccagaac      | 300 |
| Db | 241 | ctcactgtgtaacaacagtatctatcatatgctatctgtgttgccactgataccagaac      | 300 |
| QY | 301 | caccaacattgcacagtctgtgtgagagggtgttttgcactctgtgcacagtatgctctgc    | 360 |
| Db | 301 | caccaacattgcacagtctgtgtgagagggtgttttgcactctgtgcacagtatgctctgc    | 360 |
| QY | 361 | cgaacggggcccttatcttcgccggaagcttcgttcaatcccaacgcggtccctaccagaaaa  | 420 |
| Db | 361 | cgaacggggcccttatcttcgccggaagcttcgttcaatcccaacgcggtccctaccagaaaa  | 420 |
| QY | 421 | gacctgcatataaaaaaagaagctttgttaattatatactcttttagttgatatctaa       | 480 |
| Db | 421 | gacctgcatataaaaaaagaagctttgttaattatatactcttttagttgatatctaa       | 480 |
| QY | 481 | gtattaaacatatctcgtatctctccaataaaaaaataaaaaaataaaaaa 534          |     |
| Db | 481 | gtattaaacatatctcgtatctctccaataaaaaaataaaaaaataaaaaa 534          |     |

|          |                                 |
|----------|---------------------------------|
| RESULT   | 2                               |
| AAS44932 |                                 |
| ID       | AAS44932 standard; cDNA; 655 BP |
| XX       |                                 |

AC AAS44932;  
VY

DT 18-DEC-2001 (first entry)  
XX

CDNA encoding novel human secretory protein, Seq ID No 13

KM Human: secreted protein: arthritis; Crohn's disease; sepsis; shock;  
KM Ischaemia-reperfusion injury; haemaphysosis; cancer; neuropathy;  
KM transgenic animal; Alzheimer's disease; Parkinson's disease; burn;  
KM amniotrophic lateral sclerosis; platelet disorder; thrombocytopenia;  
KM ulcer; osteoporosis; bone degenerative disorder; periodontal disease  
gut protection; lung; liver fibrosis; immune deficiency; infection;

KW severe combined immunodeficiency; SCID; autoimmune disorder; allergy  
 KW multiple sclerosis; rheumatoid arthritis; diabetes mellitus; asthma;  
 KW fertility; analgesic; pain; antigen; ss.  
 XX

OS Homo sapiens.  
XY

PN WO200166689-A2  
XY

PD 13-SEP-2001.  
XX

05-MAR-2001; 2001WO-US04942.

PR 07-MAR-2000; 2000US-0519705.  
PR 19-MAY-2000; 2000US-0574454

PR 17-JUN-2000; 2000US-0596193.  
PR 14-JUL-2000; 2000US-0516947

PR 19-SEP-2000; 2000US-0665363.  
PR 20-OCT-2000; 2000US-0663367

XX  
PA (HYSE-) HYSEO INC

|    |                          |
|----|--------------------------|
| XX |                          |
| PI | Tang YT, Lin C, Asundi V |

P1 Zhao Qa, Yang Y, Drmanac R  
XX

DR P-PSDB; AAU28032.  
DR WFL; 2001-389934/66

Novel polypeptides and nucleic acids obtained from *crna 14*

Prepared from various  
cancer, neurological

PS Claim 1; SEQ ID No 13; 107bp; English

The invention relates to novel isolated human secreted polypeptides (I) and polynucleotides (II). (I) and (II) are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischaemia-reperfusion injury, shock, sepsis, immune responses, and is involved in increasing haematopoiesis, stem cell survival, bone growth and remodeling. (I), (II) and modulators of (II) are useful for prophylaxis or treatment of one or more cancers. (II) is also useful for creating transgenic animals useful for studying the *in vivo* activities of the polypeptide as well as for studying modulators of the polypeptides. (I) induces the proliferation of neural cells and regeneration of nerve and brain tissue and is useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis. In addition, (I) is involved in chemotactic or chemokinetic activity, regulation of haematopoiesis and is useful for chemokinetic and/or lymphoid cell disorders, platelet disorders such as thrombocytopenia and for regeneration of bone, cartilage, tendon, ligament and/or nerve tissue growth, and in tissue repair, healing of burns, incisions, ulcers, for treating osteoporosis, osteoarthritis, bone degenerative disorders, or periodontal disease. Furthermore, (I) is also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, various immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis, rheumatoid arthritis, diabetes mellitus, myasthenia gravis, allergic reactions and conditions, such as asthma or other respiratory problems. In addition, (I) affects biorhythms or circadian cycles of rhythms, fertility, metabolism, catabolism, anabolism, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, provides analgesic effects or other pain reducing effects, immunoglobulin like activity and can act as an antigen in a vaccine composition to raise an immune response. AAS41920-AAS45295 represent novel human secreted protein coding sequences of the invention.

Sequence 655 BP; 178 A; 129 C; 181 G; 167 T; 0 other;

|                           |         |                     |           |             |
|---------------------------|---------|---------------------|-----------|-------------|
| Query Match               | 94.9%   | Score 507;          | DB 22;    | Length 655; |
| Best Local Similarity     | 100.0%; | Pred. No. 2.7e-101; |           |             |
| Matches 507; Conservative | 0;      | Mismatches 0;       | Indels 0; | Gaps 0;     |





```

OY 76 tcgcttcgcaaacctactcagcagcagctggaagattgagggaagtgcctgc 135
    |||||||
DB 71 tcgcttcgcaaacctactcagcagcagctggaagattgagggaagtgcctgc 130
OY 136 tgggttcgcaagcagatgatacgttcagccgaataaacaatgccttcgtct 195
    |||||||
DB 131 tgggttcgcaagcagatgatacgttcagccgaataaacaatgccttcgtct 190
OY 196 caggttgaaaagcagcagatgatacgttcagccgaataaacaatgccttcgt 255
    |||||||
DB 191 caggttgaaaagcagcagatgatacgttcagccgaataaacaatgccttcgt 250
OY 256 agtattatgcctacgtatctgtgttcgactgataccagaataaacaatgcct 315
    |||||||
DB 251 agtattatgcctacgtatctgtgttcgactgataccagaataaacaatgcct 310
OY 316 tgggtgagggtgtgttcgactgataccagaataaacaatgccttcgtct 375
    |||||||
DB 311 tgggtgagggtgtgttcgactgataccagaataaacaatgccttcgtct 370
OY 376 ttaccggaagcttcgttcaatccagcagctcctaccagaataaagcctgtgc 435
    |||||||
DB 371 ttaccggaagcttcgttcaatccagcagctcctaccagaataaagcctgtgc 430
OY 436 aaaaagaatttgtaatttatattacttttaagtgtgataactaataacataatt 495
    |||||||
DB 431 aaaaagaatttgtaatttatattacttttaagtgtgataactaataacataatt 490
OY 496 ctgtattctccaaaaaataaaaaa 522
    |||||||
DB 491 ctgtattctccaaaaaataaaaaa 517

RESULT 6
AAA87730
ID AAA87730 standard; cDNA; 515 BP.
XX
AC AAA87730;
XX
DT 28-NOV-2000 (first entry)
XX
DE Human secreted protein encoding cDNA SEQ ID #29.
XX
KW Human; secreted protein; forensic procedure; gene therapy;
KW chromosome mapping; cancer; autoimmune disease; cardiovascular disorder;
KW cystic fibrosis; hypothyroidism; immunological disorder; amyloidosis;
KW brain disorder; skeletal muscle disorder; eye disorder; obesity;
KW mitochondrialopathy; diabetes; atherosclerosis; Alzheimer's disease;
KW neurodegenerative disorder; graft rejection; dementia; hyperlipidaemia;
KW septic shock; impotence; ss.
XX
XX Homo sapiens.
XX
XX OS
XX PN WO200037491-A2.
XX
XX PD 29-JUN-2000.
XX
XX PE 20-DEC-1999; 99WO-IB02058.
XX
XX PR 22-DEC-1998; 98US-0113686.
XX
XX PR 25-JUN-1999; 99US-0141032.
XX
XX PA (GENSET) GENSET.
XX
XX PI Bougueleret L, Dumas J, Duclert A.
XX
XX DR WPI: 2000-442637/38.
XX
XX DR P-PSDB; AAB25768.
XX
XX PT Polynucleotides and polypeptides encoding proteins with signal
XX peptides, useful in diagnostic, forensic, gene therapy and chromosome
XX mapping procedures -
PT

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```

XX
XX Claim 1; Page 169-170; 306pp; English.
XX
XX This sequence represents human cDNA encoding a secreted protein. The
XX invention relates to sequences AAA87725-A87774 which encode human
XX secreted proteins AAB25763-B25812. The proteins include signal peptides.
XX Included in the invention are a host cell containing one of the cDNA
XX sequences, and a purified antibody capable of binding to one of the
XX secreted proteins. Also contained in the invention are methods for
XX storing the sequence data on a computer system, and a method for
XX identifying features of the cDNA sequences using a computer programme.
XX The cDNAs are useful for expressing secreted proteins or fragments to
XX obtain antibodies capable of specifically binding to the secreted
XX proteins. The cDNAs may also be useful in diagnostic, forensic, gene
XX therapy and chromosome mapping procedures and may be used to design
XX expression vectors and secretion vectors. The proteins of the invention
XX may be used to treat diseases including cancer, autoimmune diseases,
XX cardiovascular disorders, cystic fibrosis, hypothyroidism, immunological
XX disorders, amyloidosis, brain disorders, skeletal muscle disorders, eye
XX disorders, obesity, mitochondrialopathies, diabetes, atherosclerosis,
XX neurodegenerative disorders, graft rejection, Alzheimer's disease,
XX dementia, hyperlipidaemia, septic shock and impotence.
XX
XX Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;
XX
XX
XX Query Match          92.4%; Score 493.4; DB 21; Length 515;
XX Best Local Similarity 99.4%; Pred. No. 2.4e-98;
XX Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
XX
OY 15 gtaagcagagctggcgaagaagtaagggaaggcgtgtcgcgcgcgtgtgcgt 74
    |||||||
DB 8 gggaagcagagctggcgaagaagtaagggaaggcgtgtcgcgcgcgtgtgcgt 66
OY 75 atcgttcgcaaacctactcagcagcagctggaagaagttgagggaagctgcgt 134
    |||||||
DB 67 atcgttcgcaaacctactcagcagcagctggaagaagttgagggaagctgcgt 126
OY 135 ctggtctgcagcagcagatgatacgttcgagccgaataaacaatgccttcgt 194
    |||||||
DB 127 ctggtctgcagcagcagatgatacgttcgagccgaataaacaatgccttcgt 186
OY 195 tcaagtgaagcagcagatgatacgttcgagccgaataaacaatgccttcgt 254
    |||||||
DB 187 tcaagtgaagcagcagatgatacgttcgagccgaataaacaatgccttcgt 246
OY 255 cagtatcagcagcagatgatacgttcgagccgaataaacaatgccttcgt 314
    |||||||
DB 247 cagtatcagcagcagatgatacgttcgagccgaataaacaatgccttcgt 306
OY 315 ttggtgagggtgtgttcgactgataccagaataaacaatgccttcgt 374
    |||||||
DB 307 ttggtgagggtgtgttcgactgataccagaataaacaatgccttcgt 366
OY 375 ttaccggaagcttcgttcaatccagcagctcctaccagaataaagcctgtgc 434
    |||||||
DB 367 ttaccggaagcttcgttcaatccagcagctcctaccagaataaagcctgtgc 426
OY 435 aaaaagaatttgtaatttatattacttttaagtgtgataactaataacataatt 494
    |||||||
DB 427 aaaaagaatttgtaatttatattacttttaagtgtgataactaataacataatt 486
OY 495 tctgtattctccaaaaaataaaaaa 522
    |||||||
DB 487 tctgtattctccaaaaaataaaaaa 514

RESULT 7
AAF64012
ID AAF64012 standard; cDNA; 515 BP.
XX
XX AAF64012;
XX
XX

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DT 05-APR-2001 (first entry)  
 XX cDNA encoding human secreted protein #13.  
 DE Secreted protein; prevention; treatment; diagnosis; disease;  
 XX infection; ds.  
 KW Homo sapiens.  
 OS Homo sapiens.  
 XX MO200100806-A2.  
 XX  
 XX 04-JAN-2001.  
 XX  
 XX 21-JUN-2000; 2000MO-IB00951.  
 XX  
 XX 25-JUN-1999; 99US-0141032.  
 XX 21-DEC-1999; 99US-0469099.  
 XX  
 XX (GSEST ) GENSET.  
 PA  
 PI Dumas Milne Edwards J, Bougueleret L, Jobert S;  
 DR MPI; 2001-071487/08.  
 XX  
 XX 49 Secreted proteins and the nucleic acids encoding them, useful in  
 PT gene therapy and for detecting similar sequences in samples -  
 XX  
 XX Claim 1; Page 225; 307pp; English.  
 XX  
 CC The present invention relates to 49 Secreted proteins and the cDNAs  
 CC encoding them. The protein and nucleic acids may be used in the  
 CC prevention, treatment and diagnosis of diseases associated with  
 CC inappropriate protein expression.  
 CC  
 CC Sequence 515 BP; 143 A; 106 C; 135 G; 130 T; 1 other;

Query Match 92.4%; Score 493.4; DB 22; Length 515;  
 Best Local Similarity 99.4%; Pred. No. 2.4e-98;  
 Matches 505; Conservative 0; Mismatches 2; Indels 1; Gaps 1;

QY 15 gtaagccgagcgtgggaggaagaagaaggagggcggtgtccgcgcggtgtggtct 74  
 Db 8 gggaaacccgagcgtgggaggaagaagaaggagggcggtgtccgcgcgcggtgtggtct 66  
 QY 75 atgcgttcgcaagaacctactcagcagccagcgtgagaagaagttgaggaagttgctgct 134  
 Db 67 atgcgttcgcaagaacctactcagcagccagcgtgagaagaagttgaggaagttgctgct 126  
 QY 135 ctggggtctgagcgcggtatgatacgtgcaagccgaaataaataacatgccttctgct 194  
 Db 127 ctggggtctgagcgcggtatgatacgtgcaagccgaaataaataacatgccttctgct 186  
 QY 195 tcaagtgtgaaagccagcgtgatacgtgcaagccgaaataaataacatgccttctgct 254  
 Db 187 tcaagtgtgaaagccagcgtgatacgtgcaagccgaaataaataacatgccttctgct 246  
 QY 255 cagatcatgtcatcgtatctgtgtgtgcaactgataccagaaacacacatgtgacag 314  
 Db 247 cagatcatgtcatcgtatctgtgtgtgcaactgataccagaaacacacatgtgacag 306  
 QY 315 ttgggtgaggggtgttgtaactgtgtgacagcaatgtcttctgcccaggggcccctta 374  
 Db 307 ttgggtgaggggtgttgtaactgtgtgacagcaatgtcttctgcccaggggcccctta 366  
 QY 375 ttaccggaagcttctgtcaatccagcgtctccttaacagaaagccgtgtgataaa 434  
 Db 367 ttaccggaagcttctgtcaatccagcgtctccttaacagaaagccgtgtgataaa 426  
 QY 435 aaaaagaagtttctgtaatttatattactttttagttgataactaaacataat 494  
 Db 427 aaaaagaagtttctgtaatttatattactttttagttgataactaaacataat 486

QY 495 tctgtattcttccaaaaa 522  
 Db 487 tctgtattcttccaaaaa 514  
 RESULT 8  
 ID AAV59598 standard; DNA; 504 BP.  
 XX AAV59598;  
 XX  
 XX 06-JAN-1999 (first entry)  
 XX  
 XX Human secreted protein gene 88 clone HAAV32.  
 DE  
 XX  
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW diagnosis; tissue; cancer; neurodegenerative disorder; leukoemia;  
 KW developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KW immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KW inflammation; ischaemic shock; Alzheimer's disease; restenosis; AIDS;  
 KW cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KW osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KW endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX MO9839448-A2.  
 XX  
 XX 11-SEP-1998.  
 XX  
 XX 06-MAR-1998; 98MO-US04493.  
 XX  
 XX 02-OCT-1997; 97US-0061060.  
 XX 07-MAR-1997; 97US-0038621.  
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 XX 11-APR-1997; 97US-0043672.  
 XX 11-APR-1997; 97US-0043674.  
 XX 23-MAY-1997; 97US-0047492.  
 XX 23-MAY-1997; 97US-0047500.  
 XX 23-MAY-1997; 97US-0047501.  
 XX 23-MAY-1997; 97US-0047502.  
 XX 23-MAY-1997; 97US-0047503.  
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 XX 23-MAY-1997; 97US-0047582.  
 XX 23-MAY-1997; 97US-0047583.  
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 XX 23-MAY-1997; 97US-0047585.  
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 XX 23-MAY-1997; 97US-0047590.  
 XX 23-MAY-1997; 97US-0047592.  
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 XX 23-MAY-1997; 97US-0047594.

PR 23-MAY-1997; 97US-0047595.  
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 PR 05-SEP-1997; 97US-0057659.  
 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.  
 PR XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 XX Bednarik DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA,  
 PI Peng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS,  
 PI Kyan H, Lafleur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA,  
 PI Ruben SM, Shi Y, Scoppet DR, Young PE, Yu GL, Zeng Z;  
 XX  
 DR WPI; 1998-506364/43.  
 DR P-PSDB; AAW74818.  
 XX  
 XX New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 XX

PS Claim 1; Page 320; 721pp; English.  
 XX  
 CC This sequence represents a nucleic acid molecule designated Gene 88 from  
 CC the human cDNA clone HAUAV32 (deposited as clone ATCC 97901 and ATCC  
 CC 209047) which encodes a secreted human protein. The gene can be used to  
 CC generate fusion proteins by linking to the gene to a human  
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
 CC the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-W59812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological conditions  
 CC can be diagnosed by determining the presence of mutations in the new  
 CC sample or by determining the presence of mutations in the new 186  
 CC polynucleotides. Specific uses are described for each of the new  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAV59511 for described uses).  
 CC  
 XX  
 SQ Sequence 504 BP; 143 A; 106 C; 128 G; 127 T; 0 other;

Query Match 91.1%; Score 486.6; DB 19; Length 504;  
 Best Local Similarity 99.0%; Pred. No. 7, 1e-97;  
 Matches 500; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

OY 21 ccgagctggcgagaaagtgggagggcggtctcccgccggtgtggtctatcgct 80  
 DB 1 ccgagctggcgagaaagtgggagggcggtctcccgccggtgtggtctatcgct 59  
 OY 81 tcgcagaactctactcggcgagcgagctgagaaagtgtgaggaagtgtctgtggt 140  
 DB 60 tcgcagaactctactcggcgagcgagctgagaaagtgtgaggaagtgtctgtggt 119  
 OY 141 ctgcagacgcatgagataacgtgcagcgagaaataaacatcgcccttctgtcagtg 200  
 DB 120 ctgcagacgcatgagataacgtgcagcgagaaataaacatcgcccttctgtcagtg 179  
 OY 201 tgaagggccagctgaataatgtctgggtggtatatacaactcactgttaacaacagt 260  
 DB 180 tgaagggccagctgaataatgtctgggtggtatatacaactcactgttaacaacagt 239  
 OY 261 tcatgcatcgtctcgtgtgtgtgacatgataccagaacacacacatgtgcaattgtg 320  
 DB 240 tcatgcatcgtctcgtgtgtgtgacatgataccagaacacacacatgtgcaattgtg 299  
 OY 321 gaggggtgttgcactgtgacagcagatctgtctgcagcgagggccctattacc 380  
 DB 300 gaggggtgttgcactgtgacagcagatctgtctgcagcgagggccctattacc 359  
 OY 381 ggaagctctgttcaatccagcgttcccttaacagaaagcctgtgcatgaaaaaag 440  
 DB 360 ggaagctctgttcaatccagcgttcccttaacagaaagcctgtgcatgaaaaaag 419  
 OY 441 aagtttgtaatttatatactcttttagttgatactagaattaaacatatctcgtga 500  
 DB 420 aagtttgtaatttatatactcttttagttgatactagaattaaacatatctcgtga 479  
 OY 501 ttcttccaaaaaaataaaaaaa 525  
 DB 480 ttcttccaaaaaaataaaaaaa 504

RESULT 9  
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 ID AAV59746 standard; DNA; 506 BP.  
 XX  
 AC AAV59746;  
 XX  
 DT 19-JAN-1999 (first entry)  
 XX  
 XX Human secreted protein gene 88 clone HAUAV32.  
 DE Human secreted protein; fusion protein; gene therapy; protein therapy;  
 XX Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KW

KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal; ds;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischemic shock; Alzheimer's disease; restenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 OS Homo sapiens.  
 XX  
 PN WO839448-A2.  
 XX  
 PD 11-SEP-1998.  
 XX  
 PF 06-MAR-1998; 98WO-US04493.  
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 PR 02-OCT-1997; 97US-0061060.  
 PR 07-MAR-1997; 97US-0038621.  
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 PR 23-MAY-1997; 97US-0047632.  
 PR 06-JUN-1997; 97US-0047633.  
 PR 97US-0048964.

PR 06-JUN-1997; 97US-0048974.  
 PR 13-JUN-1997; 97US-0049610.  
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 PR 22-AUG-1997; 97US-0056887.  
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 PR 22-AUG-1997; 97US-0056910.  
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 PR 05-SEP-1997; 97US-0057650.  
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 PR 05-SEP-1997; 97US-0057761.  
 PR 12-SEP-1997; 97US-0058785.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Bednarek DP, Brewer LA, Carter KC, Duan R, Ebner R, Endress GA;  
 PI Feng P, Ferlie AM, Fischer CL, Florence KA, Greene JM, Hu JS;  
 PI Kyaw H, Lallieur DW, Li Y, Moore PA, Ni J, Olsen HS, Rosen CA;  
 PI Ruben SM, Shi Y, Soppet DR, Young PE, Yu GL, Zeng Z;  
 XX WPI; 1998-506364/43.  
 DR P-PSDB; AAW74961.  
 XX  
 PT New isolated human genes and the secreted polypeptide(s) they encode  
 PT - useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 PS  
 PS Claim 1; Page 472; 721pp; English.  
 XX  
 XX This sequence represents a nucleic acid molecule designated Gene 88 from  
 CC the human CDNA clone HANUV32 (deposited as clone ATCC 97897 and ATCC  
 CC 209043) which encodes a secreted human protein. The gene can be used to  
 CC generate fusion proteins by linking to the gene to a human  
 CC immunoglobulin Fc portion (e.g. AAV59502) for increasing the stability of  
 CC the fused protein as compared to the human protein only.  
 CC The invention relates to 186 novel genes and their fragments (nucleic  
 CC acid sequences: AAV59511-V59812; amino acid sequences AAW74731-W75026)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC polypeptides in a sample or by determining the amount of the new  
 CC the new polynucleotides. Specific uses are described for each of the 186  
 CC polynucleotides, based on which tissues they are most highly expressed in





|    |                               |
|----|-------------------------------|
| OS | Homo sapiens.                 |
| XX |                               |
| PN | MO200005367-A2.               |
| XX |                               |
| PD | 03-FEB-2000.                  |
| XX |                               |
| PF | 22-JUL-1999; 99WO-JP03929.    |
| XX |                               |
| PR | 24-JUL-1998; 98JP-0208820.    |
| PR | 07-AUG-1998; 98JP-0224105.    |
| PR | 25-AUG-1998; 98JP-0238116.    |
| PR | 09-SEP-1998; 98JP-0254736.    |
| PR | 29-SEP-1998; 98JP-0275505.    |
| XX |                               |
| PA | (SAGA ) SAGAMI CHEM RES CENT. |
| PA | (PROT-) PROTEGENE INC.        |
| XX |                               |
| PI | Kato S, Kimura T;             |
| XX |                               |
| DR | WPI: 2000-182694/16.          |
| DR | P-PSDB: AAV94861.             |
| XX |                               |

This sequence encodes a human protein of the invention, which has hydrophobic domains. The DNA sequences can be used as a probe or as a genetic marker. The protein can also be used as a marker, and to identify potential genetic disorders. The DNA and protein can also be used as nutritional sources or supplements. The protein exhibits cytokine, cell proliferation, cell differentiation activities and induces production of immune stimulating or immune suppressing activity. It can be used in the treatment of various immune deficiencies and disorders, and to treat infectious diseases caused by viral, bacterial, fungal or other infections. The protein is also used for treating autoimmune disorders such as multiple sclerosis, systemic lupus erythematosus, and rheumatoid arthritis. It is also useful in the treatment of allergic reactions and conditions such as asthma, and in immune suppression after organ transplantation. The protein is useful in regulation of hematopoiesis and consequently in the treatment of myeloid or lymphoid cell deficiencies. It is also used in compositions for tissue growth or regeneration. The protein is also used in the treatment of osteoporosis or osteoarthritis and in the treatment of periodontal disease and other tooth repair processes. The protein is used in the treatment of nervous system disorders such as Alzheimer's disease, Parkinson's disease, and Huntington's disease. They are useful for protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage. They are also used for promoting or inhibiting tissue differentiation. They are also used as contraceptives since they exhibit activin or inhibin related activities and as a fertility inducing therapeutic. They are used for treating various coagulation disorders and in treatment and prevention of conditions resulting from coagulation activities e.g. myocardial infarction or stroke. They also acts as receptors, receptor ligands or inhibitors or agonists of receptor/ligand interactions. They are used to treat inflammatory conditions such as septic shock, sepsis, ischaemia

(GEST ) GENSET  
13-APR-1998; 98US-0081563.  
10-AUG-1998; 98US-0096116.

(GEST ) GENSET



DT 07-DEC-1999 (first entry)  
 XX Human PRO772 nucleotide sequence.  
 XX Human: PRO: EST: expressed sequence tag; PCR primer; hybridisation;  
 KM probe; blood coagulation disorder; cancer; cellular adhesion disorder;  
 KM secreted protein; transmembrane protein; ss.  
 XX Homo sapiens.  
 PN MO9946281-A2.  
 PD 16-SEP-1999.  
 XX 08-MAR-1999; 99WO-US05028.  
 PF 10-MAR-1998; 98US-0077450.  
 PR 11-MAR-1998; 98US-0077632.  
 PR 11-MAR-1998; 98US-0077641.  
 PR 11-MAR-1998; 98US-0077791.  
 PR 12-MAR-1998; 98US-0078004.  
 PR 13-MAR-1998; 98US-0040220.  
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 PR 31-MAR-1998; 98US-0080194.  
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 PR 28-APR-1998; 98US-0083392.  
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 PR 30-APR-1998; 98US-0083742.

PR 05-MAY-1998; 98US-0084366.  
 PR 06-MAY-1998; 98US-0084414.  
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 PR 13-MAY-1998; 98US-0085233.  
 PR 13-MAY-1998; 98US-0085338.  
 PR 13-MAY-1998; 98US-0085339.  
 PR 15-MAY-1998; 98US-0085573.  
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 PR 28-MAY-1998; 98US-0087106.  
 PR 30-JUL-1998; 98US-0087208.  
 PR 11-SEP-1998; 98US-0094651.  
 XX (GENE ) GENENTECH INC.  
 PA Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;  
 XX WPI; 1999-551358/46.  
 DR P-PSDB; AAY41713.  
 XX New secreted and transmembrane polypeptides and their polynucleotides,  
 PT useful for treating blood coagulation disorders, cancers and cellular  
 PT adhesion disorders -  
 XX  
 PS Claim 2; Fig 69; 530pp; English.  
 XX

CC The present invention describes secreted and transmembrane polypeptides  
 CC and their polynucleotides. The nucleotide sequences are useful as  
 CC sources of probes, primers, for chromosome mapping, and for generation  
 CC of antisense sequences. They can also be used to create transgenic  
 CC animals. The proteins can be used to treat a variety of diseases and  
 CC disorders, depending on their function. Diseases that may be treated  
 CC include blood coagulation disorders, cancers and cellular adhesion  
 CC disorders. They may also be used to raise antibodies. AA33891 to  
 CC AA33338, and AAY41685 to AAY41774 represent polynucleotide and  
 CC polypeptide sequence given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 663 BP; 180 A; 137 C; 153 G; 193 T; 0 other;

Query Match 62.7%; Score 335; DB 20; Length 663;  
 Best Local Similarity 76.0%; Pred. No. 7.4e-64;  
 Matches 504; Conservative 0; Mismatches 0; Indels 159; Gaps 1;  
 QY 22 cgaagctgggagaaaggaagggagggcggtgctccgcgcggtggcggtgtctatcgctt 81  
 DB 1 cgaagctgggagaaaggaagggagggcggtgctccgcgcggtggcggtgtctatcgctt 60  
 QY 82 cgaagaactactcaggaacacccagctgagaaggtttagggaaagtctctgtctggtc 141  
 DB 61 cgaagaactactcaggaacacccagctgagaaggtttagggaaagtctctgtctggtc 120  
 QY 142 tgcagagcgcgagtgtgataacgttcagccggaataaataacatcgccttcgtctcagtgt 201





GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Run on:      July 17, 2002, 07:02:45 ; Search time 77.95 Seconds
              (without alignments)
              1682.723 Million cell updates/sec
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| Title:         | US-09-801-115-1                                  |
| perfect score: | 534  |
| Sequence:      | 1 gttcccaatctgaatgaag.....aaaaaaaaaaaaaaaaaa 534 |

Scoring table:

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|              | IDENTITY | GAPOP      |
| Gapop 10.0 , |          | Gapext 1.0 |

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: /6/066

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000

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post-processing:  Minimum Match 0%
                  Maximum Match 100%
                  Listing first 45 summaries

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5: /cgn2_6/ptodata/2/ina/PCrUs.COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfile1.seq.*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID                | Description        |
|------------|-------|-------------|--------|----|-------------------|--------------------|
| 1          | 27.2  | 50.9        | 392    | 4  | US-09-385-982-95  | Sequence 95, Appl  |
| 2          | 50.4  | 9.4         | 1582   | 3  | US-08-545-1968-10 | Sequence 10, Appl  |
| 3          | 50.4  | 9.4         | 1582   | 3  | US-08-545-1968-12 | Sequence 12, Appl  |
| 4          | 46.8  | 8.8         | 770    | 3  | US-08-865-297-5   | Sequence 5, Appl   |
| 5          | 45.8  | 8.6         | 3761   | 4  | US-08-890-865A-2  | Sequence 2, Appl   |
| 6          | 45    | 8.4         | 961    | 6  | 5194596-16        | Patent No. 5194596 |
| 7          | 45    | 8.4         | 961    | 6  | 5219739-16        | Patent No. 5219739 |
| 8          | 44.6  | 8.4         | 2920   | 3  | US-09-276-400-1   | Sequence 1, Appl   |
| 9          | 44.6  | 8.4         | 2920   | 4  | US-09-448-076-1   | Sequence 1, Appl   |
| 10         | 44.4  | 8.3         | 333    | 3  | US-08-946-026-35  | Sequence 35, Appl  |
| 11         | 44.2  | 8.3         | 581    | 2  | US-08-557-309B-22 | Sequence 22, Appl  |
| 12         | 44.2  | 8.3         | 581    | 3  | US-08-834-306-22  | Sequence 22, Appl  |
| 13         | 44.2  | 8.3         | 581    | 4  | US-08-993-674A-22 | Sequence 22, Appl  |
| 14         | 43    | 8.1         | 2589   | 4  | US-08-563-749-1   | Sequence 1, Appl   |
| 15         | 43    | 8.1         | 2589   | 5  | PCT-US96-12860-1  | Sequence 1, Appl   |
| 16         | 43    | 8.1         | 3238   | 4  | US-08-123-934A-5  | Sequence 5, Appl   |
| 17         | 43    | 8.1         | 3238   | 5  | PCT-US94-10080-5  | Sequence 5, Appl   |
| 18         | 42.8  | 8.0         | 1332   | 2  | US-09-057-762-1   | Sequence 1, Appl   |
| 19         | 42.8  | 8.0         | 1332   | 2  | US-08-326-119A-1  | Sequence 1, Appl   |
| 20         | 42.8  | 8.0         | 3471   | 5  | PCT-US93-00227-2  | Sequence 2, Appl   |
| 21         | 42    | 7.9         | 940    | 2  | US-08-471-717-1   | Sequence 1, Appl   |
| 22         | 41.8  | 7.8         | 742    | 1  | US-07-847-010-12  | Sequence 12, Appl  |
| 23         | 41.4  | 7.8         | 5852   | 1  | US-07-867-106-2   | Sequence 2, Appl   |
| 24         | 41.2  | 7.7         | 2671   | 6  | 5168051-9         | Patent No. 5168051 |
| 25         | 41.2  | 7.7         | 3459   | 2  | US-08-080-060-3   | Sequence 3, Appl   |
| 26         | 41.2  | 7.7         | 3459   | 4  | US-09-307-185-3   | Sequence 3, Appl   |
| 27         | 40.8  | 7.6         | 1046   | 1  | US-08-361-467B-4  | Sequence 4, Appl   |

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| 28 | 40.8 | 7.6 | 1046 | 1 | US-08-484-335C-2  | Sequence 2, Appl1  |
| 29 | 40.6 | 7.6 | 731  | 1 | US-08-484-405A-2  | Sequence 2, Appl1  |
| 30 | 40.6 | 7.6 | 2444 | 3 | US-08-906-791-1   | Sequence 1, Appl1  |
| 31 | 40.6 | 7.6 | 766  | 1 | US-09-245-041-18  | Sequence 18, Appl1 |
| 32 | 40.4 | 7.6 | 2625 | 4 | US-08-591-639-1   | Sequence 1, Appl1  |
| 33 | 40.4 | 7.6 | 1253 | 2 | US-08-781-420-10  | Sequence 10, Appl1 |
| 34 | 40.4 | 7.6 | 1472 | 4 | US-08-874-102-10  | Sequence 12, Appl1 |
| 35 | 40.4 | 7.6 | 1472 | 4 | US-08-874-102-12  | Sequence 10, Appl1 |
| 36 | 40.4 | 7.6 | 1472 | 4 | US-08-874-102-10  | Sequence 12, Appl1 |
| 37 | 40.4 | 7.6 | 1472 | 4 | US-08-874-102-12  | Sequence 10, Appl1 |
| 38 | 40.4 | 7.6 | 1881 | 4 | US-08-874-102-46  | Sequence 46, Appl1 |
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| 40 | 40.4 | 7.6 | 2007 | 3 | US-08-747-221B-36 | Sequence 36, Appl1 |
| 41 | 40.4 | 7.6 | 2007 | 3 | US-08-747-221B-36 | Sequence 36, Appl1 |
| 42 | 40.4 | 7.6 | 2007 | 4 | US-09-005-051-36  | Sequence 36, Appl1 |
| 43 | 40.4 | 7.6 | 2007 | 4 | US-09-005-051-38  | Sequence 38, Appl1 |
| 44 | 40.2 | 7.5 | 2217 | 4 | US-09-244-314-12  | Sequence 1, Appl1  |
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## ALIGNMENTS

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50.98; Score 272; DB 4; Length 392;

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| QY      | 286  | actcgataccaagaaccacacacattgacagtgtgtggaagggtgttgcactgttgacgc      | 345 |
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| QY      | 103  | actgataccaagaaccacacacattgacagtgtgtggaagggtgttgcactgttgacgc       | 162 |
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| Db      | 406  | tccttaaccagaaaagccttgcgtgacgtgaaataaagaagtttgttaatttataactt       | 464 |

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Db 283 nttaagttgatactaaacatactctgtatcttccaaaaa 342  
Oy 524 aaaaaaa 534  
Db 343 tnaantanaa 353

## RESULT 2

US-08-545-196B-10  
Sequence 10, Application US/08545196B  
Patent No. 6080577  
GENERAL INFORMATION:  
APPLICANT: MELKI, JUDITH  
APPLICANT: MURNICH, ARNOLD  
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE  
TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,196B  
FILING DATE: 19-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FARACI, C. J.  
REGISTRATION NUMBER: 32,350  
REFERENCE/DOCKET NUMBER: 2121-110P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-545-196B-10

Query Match 9.4%; Score 50.4; DB 3; Length 1582;  
Best Local Similarity 71.7%; Pred. No. 0.0006;  
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Oy 443 gtttgtaatttatattacttttgaatgaactaagaatataatctgtat 502  
Db 1427 gtttgtaatttatattacttttgaatgaactaagaatataatctgtat 502  
Oy 503 ctcccaaaaaa 534  
Db 1487 ttttaaaaaa 1518

## RESULT 3

US-08-545-196B-12  
Sequence 12, Application US/08545196B  
Patent No. 6080577  
GENERAL INFORMATION:  
APPLICANT: MELKI, JUDITH  
APPLICANT: MURNICH, ARNOLD  
TITLE OF INVENTION: SURVIVAL MOTOR NEURON (SMN) GENE: A GENE

TITLE OF INVENTION: FOR SPINAL MUSCULAR ATROPHY  
NUMBER OF SEQUENCES: 65  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH, LLP  
STREET: PO BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/545,196B  
FILING DATE: 19-OCT-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: FARACI, C. J.  
REGISTRATION NUMBER: 32,350  
REFERENCE/DOCKET NUMBER: 2121-110P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1582 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-545-196B-12

Query Match 9.4%; Score 50.4; DB 3; Length 1582;  
Best Local Similarity 71.7%; Pred. No. 0.0006;  
Matches 66; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

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Db 1427 gtttgtaatttatattacttttgaatgaactaagaatataatctgtat 502  
Oy 503 ctcccaaaaaa 534  
Db 1487 ttttaaaaaa 1518

## RESULT 4

US-08-865-297-5  
Sequence 5, Application US/08865297  
Patent No. 6010853  
GENERAL INFORMATION:  
APPLICANT: Prasad V. S. Kanteti, Zhaochui Ao, and Stuart F.  
TITLE OF INVENTION: The Siva Genes, No. 6010853el Genes Involved in  
TITLE OF INVENTION: C027-mediated Apoptosis  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: LAHIVE & COCKFIELD, LLP  
STREET: 60 State Street, Suite 510  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02109-1875  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/865,297  
FILING DATE: 29-MAY-1997



RESULT 7  
 5219739-16  
 Patent No. 5219739  
 APPLICANT: TISCHER, EDMUND G.; ABRAHAM, JUDITH A.; FIDDES,  
 JOHN C.; MITCHELL, RICHARD L.  
 TITLE OF INVENTION: DNA SEQUENCES ENCODING BVGF120 AND  
 BVGF121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN  
 BVGF121 AND METHODS FOR THE PRODUCTION OF BOVINE AND HUMAN  
 BVGF120 AND BVGF121  
 VASCULAR ENDOTHELIAL CELL GROWTH FACTORS, BVGF120 AND BVGF121  
 NUMBER OF SEQUENCES: 40  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: 05/07/559,041  
 FILING DATE: 27-JUL-1990  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 450,883  
 FILING DATE: 14-DEC-1989  
 APPLICATION NUMBER: 387,545  
 FILING DATE: 27-JUL-1989  
 SEQ ID NO:16:





REGISTRATION NUMBER: 31,392  
REFERENCE/DOCKET NUMBER: 210121.422C2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 622-4900  
TELEFAX: (206) 682-6031  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 581 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-993-674A-22

Query Match 8.3%; Score 44.2; DB 4; Length 581;  
Best Local Similarity 68.5%; Pred. No. 0.015;  
Matches 61; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 446 ttgtaatttatacttctttagttgataactaagtaataacataattctgtatctt 505  
Db 484 ttttttttattgtcttttttttttttttttttttttttttttttttttttttt 543  
QY 506 ccaaaaaaaaaaaaaaaaaaaaaa 534  
Db 544 CAAAAAAAAAAAAAAAAAAAAA 572

## RESULT 14

US-08-569-749-1  
Sequence 1, Application US/08569749  
Patent No. 6187557

## GENERAL INFORMATION:

APPLICANT: Roche, Mike  
APPLICANT: Goedel, David V  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:

ADDRESS: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/569,749  
FILING DATE:

## CLASSIFICATION: 514

## ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2589 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-569-749-1

Query Match 8.1%; Score 43; DB 4; Length 2589;  
Best Local Similarity 64.6%; Pred. No. 0.057;  
Matches 64; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 436 aaaaagaatttgytaattatatactttagtttgataactaagtaataacataatt 495  
Db 2468 AAAATAAGGATTTTCTCTATTTCCTCCCTAGTTGTGAGAAACATCTCAATAAAGTG 2527  
QY 496 ctgtatcttcacaaaaaaaaaaaaaaaaaaaaa 534  
Db 2528 CTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2566

## RESULT 15

PCT-US96-12860-1  
Sequence 1, Application PC/TUS9612860  
GENERAL INFORMATION:

APPLICANT: TULARIC, INC.  
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT  
STREET: 4 Embarcadero Center, Suite 3400  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/12860  
FILING DATE: 06 AUG 1996  
CLASSIFICATION:

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749  
CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:  
NAME: Brezner, David J.  
REGISTRATION NUMBER: 24,774  
REFERENCE/DOCKET NUMBER: A-62464/DJB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415)781-1989  
TELEFAX: (415)398-3249

## INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:  
LENGTH: 2589 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
PCT-US96-12860-1

Query Match 8.1%; Score 43; DB 5; Length 2589;  
Best Local Similarity 64.6%; Pred. No. 0.057;  
Matches 64; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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Db 2468 AAAATAAGGATTTTCTCTATTTCCTCCCTAGTTGTGAGAAACATCTCAATAAAGTG 2527  
QY 496 ctgtatcttcacaaaaaaaaaaaaaaaaaaaaa 534  
Db 2528 CTTTAAAAAAAAAAAAAAAAAAAAAAAAA 2566

Search completed: July 17, 2002, 09:25:08  
Job Time: 8543 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:05:10 ; Search time 1859.31 Seconds  
(without alignments)  
6010.171 Million cell updates/sec

Title: US-09-801-115-1  
534  
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Sequence:

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: gb\_hcg:\*  
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4: gb\_om:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_mu:\*  
21: em\_ov:\*  
22: em\_ov:\*  
23: em\_pat:\*  
24: em\_ph:\*  
25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result NO. | Score | Query Match | Length | ID | Description |
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| 3  | 349.4 | 65.4 | 689    | 9  | AF135380   |
| 4  | 349   | 65.4 | 593    | 9  | AF145216   |
| 5  | 338   | 63.3 | 688    | 9  | BC004380   |
| 6  | 325.4 | 60.9 | 655    | 9  | AF057306   |
| 7  | 321.8 | 60.3 | 669    | 6  | AX061665   |
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| 9  | 278   | 52.1 | 485    | 11 | G30204     |
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| 12 | 214.4 | 40.1 | 188460 | 2  | AC010542   |
| 13 | 205   | 38.4 | 207    | 6  | AX330610   |
| 14 | 205   | 38.4 | 207    | 6  | AX330787   |
| 15 | 205   | 38.4 | 207    | 6  | AX331008   |
| 16 | 185.2 | 34.7 | 455    | 6  | AX079435   |
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| 21 | 158.4 | 29.7 | 6283   | 6  | AX348836   |
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| 24 | 119.4 | 22.4 | 6283   | 6  | AX344430   |
| 25 | 119.4 | 22.4 | 6283   | 6  | AX348835   |
| 26 | 119.4 | 22.4 | 6283   | 6  | AC000090   |
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| 28 | 63.8  | 11.9 | 527    | 10 | BC008268   |
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| 32 | 50.6  | 9.5  | 2165   | 9  | BC009565   |
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| 35 | 50.4  | 9.4  | 1582   | 6  | A77035     |
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| 40 | 50    | 9.4  | 2483   | 3  | DDI13A     |
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| 42 | 49.6  | 9.3  | 1345   | 10 | BC011306   |
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| 44 | 49.6  | 9.3  | 169794 | 2  | AC004688   |
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## ALIGNMENTS

| RESULT     | 1  | 530 bp | mrna | linear | PRI 18-JUL-2001 |
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| LOCUS      | AF096895   |        |      |        |                 |
| DEFINITION | Homo sapiens chemokine-like factor 1 (CKLF1) mRNA, complete cds.   |        |      |        |                 |
| ACCESSION  | AF096895.2   |        |      |        |                 |
| VERSION    | AF096895.2   |        |      |        |                 |
| KEYWORDS   | FLI-CDNA.  |        |      |        |                 |
| SOURCE     | human.   |        |      |        |                 |
| ORGANISM   | Homo sapiens   |        |      |        |                 |
| REFERENCE  | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.                                |        |      |        |                 |
| AUTHORS    | Han, W., Lou, Y., Tang, J., Zhang, Y., Chen, Y., Li, Y., Gu, W., Huang, J., Xia, D., Rui, W., Tang, J., and Ma, D.   |        |      |        |                 |
| TITLE      | Molecular cloning and characterization of chemokine-like factor 1 (CKLF1), a novel human cytokine with unique structure and potential chemotactic activity |        |      |        |                 |
| JOURNAL    | Biochem J. 357 (Pt 1), 127-135 (2001)  |        |      |        |                 |
| MEDLINE    | 2308461  |        |      |        |                 |
| PUBMED     | 11415443   |        |      |        |                 |
| REFERENCE  | 2 (bases 1 to 530)   |        |      |        |                 |
| AUTHORS    | Han, W., Lou, Y., Tang, J., Zhang, Y., Chen, Y., Li, Y., Gu, W., Huang, J., Xia, D., Rui, W., Tang, J., and Ma, D.   |        |      |        |                 |

TITLE Direct Submission  
JOURNAL Submitted (03-OCT-1998) Immunology, Beijing Medical University, 38  
REFERENCE Xue Yuan Rd., Beijing 100083, China  
AUTHORS 3 (bases 1 to 530)  
TITLE Han, W.L.  
JOURNAL Direct Submission  
SUBMITTED (07-SEP-2000) Immunology, Peking University Health  
Science Center, Xueyuan Road 38, Beijing 100083, China  
REMARK Sequence update by submitter  
COMMENT On Sep 7, 2000 this sequence version replaced g1:628733.  
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Query Match 97.1%; Score 518.4; DB 9; Length 530;  
Best Local Similarity 99.8%; Pred. No. 2.3e-116;  
Matches 519; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
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RESULT 2  
LOCUS AX061624  
DEFINITION Sequence 29 from Patent WO0100806.  
ACCESSION AX061624  
VERSION AX061624.1 GI:12406709  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 515)  
AUTHORS dumas milne Edwards, J.B., Bougueret, L. and Jobert, S.  
TITLE Complementary dna's encoding proteins with signal peptides  
JOURNAL Patent: WO 0100806-A 29 04-JAN-2001;  
GENSET (FR)

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Best Local Similarity 99.4%; Pred. No. 3e-110;  
Matches 503; Conservative 0; Mismatches 2; Indels 1; Gaps 1;  
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QY 135 ctgggtctgcagacgcgagtgtgtaacgtgcagccgaaataaacaatgcgccttctgt 194  
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QY 195 tcaatgtgaagccagctgaagatgtcgtggtggtggtatataccaactcactgttaaca 254  
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QY 375 ttaccggaagcctctgttcaatcccaagcggtctcaccagaagaagcctgtgacgaa 434  
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[illegible]

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QY 230 ----- 229  
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| RESULT      | 7   | AX061665     | LOCUS     | AX061665   | Sequence 70 from Patent WO0100806. | 669 bp | DNA | linear | PAT 24-JAN-2001 |
|-------------|---|--------------|-----------|--|------------------------------------|--------|-----|--------|-----------------|
| DEFINITION  | AX061665  |              | ACCESSION | AX061665   |                                    |        |     |        |                 |
| VERSION     | AX061665.1  | GI:12406789  | KEYWORDS  |  |                                    |        |     |        |                 |
| SOURCE      | human.  |              | ORGANISM  | Homo sapiens   |                                    |        |     |        |                 |
| REFERENCE   | Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;      |              | AUTHORS   | Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo. |                                    |        |     |        |                 |
| TITLE       | 1 (bases 1 to 669)  |              | JOURNAL   | dumas mlme Edwards, J. B., Bougueleret, L. and Joberet, S. |                                    |        |     |        |                 |
|             | Complementary dna's encoding proteins with signal peptides            |              |           | Patent: WO 0100806-A 70 04-JAN-2001;                       |                                    |        |     |        |                 |
| FEATURES    | GENSET (FR)   |              | source    | Location/Qualifiers  |                                    |        |     |        |                 |
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|             | 655..669  |              |           |  |                                    |        |     |        |                 |
| BASE COUNT  | 178 a   | 139 c        | 158 g     | 194 t  |                                    |        |     |        |                 |
| ORIGIN      |   |              |           |  |                                    |        |     |        |                 |
| Query Match | 60.3%   | Score 321.8; | DB 6;     | Length 669;  |                                    |        |     |        |                 |

Best Local Similarity 75.6%; Pred. No. 2.7e-68;  
Matches 504; Conservative 0; Mismatches 2; Indels 161; Gaps 2;

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QY 15 gtgaagccgaagctggcgagaaagtaaggagcgatctccggcgagggcggtgtct 74
Db 5 GGGAAAGCCGAGCTGGCGAGAGTAGGAGGCGGCGCTCCGCGCGGCGGCTTGTCT 74
QY 75 atgccttcgagaaacctactcaagcagcagctgagaaaggttgaaggaaagtcgtct 64
Db 65 ATGCGCTTCGAGAGAACTACTCAGGACCGACGAGAGAGTTGAGAGG--ATTGCTGCTG 122
QY 135 ctgggtctgagagcggatgataacgttcagcgcgaataaacaatccgccccttctgt 194
Db 123 CTGGGCTCTGACAGCGGAGTAGATACGTGACCGCAAAATAAACCTCCCTCTCTGCT 182
QY 195 tcaagtgaaagcgacgagatgctcgagctg----- 229
Db 183 TCAAGTGTGAAAGCCGACGTAAGATGCTCGGCTGCGACTAAGTGTGACATCTATGACCT 242
QY 230 ----- 229
Db 243 TTTTATCATGCGACACGCCCTGACCATATATTGTATCATCGGATTTGAAGTCACCG 302
QY 230 ----- 229
Db 303 TTATCTATTTTTCATACTTTTATATGACTGACACTTGATCGATTAATGAAGGTAT 362
QY 230 ----- 229
Db 363 TTTGCGCTTTGCTTGATATTAATCACTCACTGTAACACAGATATCATCTCATCTAT 422
QY 276 ctgtgttgagacgtgataccgaacaacatcagatgagtgagaggggtgttgcac 335
Db 423 CTGTGTGGACAGTGAACACGAAACCAACATGACAGTTGGTGAAGGGGTGTTGAC 482
QY 336 ttgtgacagcagatgctctctgagcaggggccccttattaccggaaagcttcgttca 395
Db 483 TTGTGACACAGATGCTCTCTTCCGACGGGGCCCTTATTTTACCGAGCTTCTGTTCA 542
QY 396 atcccgagcgctctcactcaagaaagcctgtgcatgaaataaagaatttgaattt 455
Db 543 ATCCCAAGCGGCTCTTACAGAAAGAGCTGTGACGAAAGAAAGAGTTTGAATTTT 602
QY 456 atattactttttagttatatacagtaataatatttctgtatcttccaaaaaaa 515
Db 603 ATATTACTTTTGTAGTTGATTAAGTATTTAACATATTCTGTATTCTCCAAAAAAA 662
QY 516 aaaaaa 522
Db 663 AAAAAA 669

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RESULT 8  
AF135381 434 bp mRNA linear PRI 07-SEP-2000  
LOCUS AF135381 Homo sapiens chemokine-like factor 3 (CKLF3) mRNA, complete cds,  
DEFINITION AF135381 alternative spliced.  
ACCESSION AF135381.2 GI:9989693  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM human.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
AUTHORS Han, W. L., Gu, W., Li, Y., Zhang, Y., Song, Q., Di, C. and Ma, D.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAR-1999) Immunology, Beijing Medical University, Xue  
Yuan Road, Beijing 100083, China  
2 (bases 1 to 434)  
Han, W. L.  
Direct Submission  
Submitted (07-SEP-2000) Immunology, Peking University Health

REMARK Science Center, Xueyuan Road 38, Beijing 100083, China  
COMMENT Sequence update by submitter  
On Sep 7, 2000 this sequence version replaced gi:6630855.  
FEATURES  
source  
1..434  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/cell\_line="937"  
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1..434  
/gene="CKLF3"  
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/note="TUCR"  
148..351  
/gene="CKLF3"  
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/codon\_start=1  
/product="chemokine-like factor 3"  
/protein\_id="AF19600.1"  
/db\_xref="GI:6630856"  
/translation="MDNVPKIKHRPFCRSVKGHVKMLRFLVATVAVCLADGALIV  
RLLFNPSPYOKKPYHEKEVY"  
BASE COUNT 127 a 88 c 116 g 103 t  
ORIGIN

Query Match 59.3%; Score 316.4; DB 9; Length 434;  
Best Local Similarity 81.3%; Pred. No. 5.1e-67;  
Matches 423; Conservative 0; Mismatches 1; Indels 96; Gaps 1;  
QY 15 gtgaagccgaagctggcgagaaagtaaggagcgatctccggcgagggcggtgtct 74  
Db 11 GGGAAAGCCGAGCTGGCGAGAGTAGGAGGCGGCGCTCCGCGCGGCGGCTTGTCT 70  
QY 75 atgccttcgagaaacctactcaagcagcagctgagaaaggttgaaggaaagtcgtct 134  
Db 71 ATGCGCTTCGAGAGAACTACTCAGGACCGACGTAAGAGTTGAGGAAAGTGTCTGCT 130  
QY 135 ctgggtctgagagcggatgataacgttcagcgcgaataaacaacatccgccccttctgt 194  
Db 131 CTGGGCTCTGACAGCGGAGTAGATACGTGACCGCAAAATAAACATTCGCTCTGCT 190  
QY 195 tcaagtgaaagcgacgagatgataacgttcagcgcgaataaacaacatccgccccttctgt 194  
Db 191 TCAAGTGTGAAAGCCGACGTAAGATGCTCGGCT----- 224  
QY 225 cagttatcgtcctcagtcgtatctgttgcacgtgataccagaacacacatgacag 314  
Db 225 ----- 224  
QY 315 ttggtgaggggtgttgcactgtgagcagatgctgtcttgcagcggggccctta 374  
Db 225 -----GCTGTTTCACCTTGTGACAGAGTATGCTGCTTGGCCAGCGGCGCTTA 274  
QY 375 ttaccggaagcttctgttcaatcccaagcgttccttaccagaataaagcgtgtgataaa 434  
Db 275 TTTACCGGAGCTCTGTTCAATCCAGCGGCTCTTACAGAAAGAGCTGTGATGATAA 334  
QY 435 aaaaagaagcttctgtaattatatactttagttgagtaagtaagtaataatatt 494  
Db 335 AAAAAGAGTTTGTATTATTTTATTATTCTTTTGAAGTTGATTAAGTATTATT 394  
QY 495 tctgtatcttccaaaaaataaataaataaataaataa 534  
Db 395 TCTGTATTCTTCCAAAAAATAAATAAATAAATAAATAA 434

RESULT 9  
G30204/c 485 bp DNA linear STS 05-OCT-1996  
LOCUS G30204 human STS SHC-36487, sequence tagged site.  
DEFINITION G30204  
ACCESSION G30204.1 GI:1593755  
VERSION  
KEYWORDS STS; STS sequence; primer; sequence tagged site.

SOURCE human.  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
JOURNAL 1 (bases 1 to 485)  
COMMENT Myers, R.M.  
Unpublished (1996)

Contact: Richard M. Myers  
Stanford Human Genome Center (SHGC)  
Stanford University School of Medicine  
Department of Genetics, M-344, Stanford, CA 94305, USA  
Tel: 4157259687  
Fax: 4157259689  
Email: myers@shgc.stanford.edu

Primer A: ACTCTCTTTTTCATGCACAGC  
Primer B: GCCCTATTACCGAAGCT  
STS size: 77  
PCR Profile:

Initial incubation: 94 degrees C for 90 seconds  
Denaturation: 94 degrees C for 15 seconds  
Annealing: 62 degrees C for 23 seconds  
Polymerization: 72 degrees C for 30 seconds  
PCR Cycles: 30  
Thermal Cycler: Perkin Elmer 9600  
Protocol:  
Template: 25 ng  
each 1 uM  
dNTPs: each 200 uM  
Tag Polymerase: 0.05 units/uL  
Total Vol: 10 uL

Buffer: MgCl2: 2.5 mM  
KCl: 50 mM  
Tris-HCl: 20 mM  
pH: 8.3

Prepared with primer pairs provided by Sandoz, derived from T90569  
-- Washington University/Merck EST sequence.

## FEATURES

## source

1.485  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/map="16"

## STS

primer\_bind  
complement(126..145)

BASE COUNT 146 a 99 c 99 g 131 t 10 others

## ORIGIN

Query Match 52.1%; Score 278; DB 11; Length 485;  
Best Local Similarity 97.9%; Pred. No. 1.3e-57;  
Matches 261; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 226 gctgagatataactactactgtaacacagatattatcgtatctgtgtggtgc 285  
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Db 287 GCTTGATATATCAACACACATGTAACACAGATATCATGCTCATGCTANCTGTGGC 228  
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QY 286 acgagaccagaaacacacacattgacagttggtggaagggtgttgcactgtgacagc 345  
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Db 227 ACTGATACCAAGAACCAACACATTGACAGTTGGAGAGGGGTGTTGCACTTGAGACAGC 168  
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QY 346 agtatagtctcttcgcagcaggggccctattattacaggaaagcttgttcaatccacgagc 405  
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Db 167 AGTATGCTGCTTTCGCCGCGGCGCTTATTTACCGAAGCTTGTTCAATCCACGCG 108  
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QY 406 tccttaccagaaaagcgtgtgcatgnaaaaaaagaagtttgttaatttatattactt 465  
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Db 107 TCCTTACCGAAGAACGCTGTGATGAAAAAAGAAAGTTTGTATTTTATTTACTTT 48  
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OY 466 ttagtgtactactaagratataacatattctgtatcttccaaaa 512  
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Db 47 TTAGTTGATAGTAAGTATTAACATATTCTGTATTTCTAATAATAA 1  
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RESULT 10  
AC010289/c 97083 bp DNA linear PRI 06-SEP-2001  
LOCUS  
DEFINITION Homo sapiens chromosome 16 clone CTA-989F12, complete sequence.  
AC010289  
VERSION AC010289.9 GI:15451657  
KEYWORDS HTG.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS 1 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS 2 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
3 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS Submitted (24-OCT-2000) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
4 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS Submitted (09-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
5 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS Submitted (10-AUG-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
6 (bases 1 to 97083)  
TITLE DOE Joint Genome Institute and Stanford Human Genome Center.  
JOURNAL Direct Submission

REFERENCE  
AUTHORS Submitted (06-SEP-2001) DOE Joint Genome Institute, 2800 Mitchell  
Drive, Walnut Creek, CA 94598, USA  
On Sep 6, 2001 this sequence version replaced g1:15147148.  
Draft Sequence. Produced by DOE Joint Genome Institute  
www.jgi.doe.gov

Finishing Completed at Stanford Human Genome Center  
www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.8% of Sequence;  
Estimated Total Number of Errors is 0.2.  
STS Content:  
WI-11439 G23701  
WI-15863 G24307  
WI-11780 G23805  
NOTE: A bacterial transposon was excised from this clone at  
position 96045.

## FEATURES

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1.97083  
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/db\_xref="taxon:9606"  
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BASE COUNT 22777 a 23172 c 24521 g 26613 t

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Query Match 40.1%; Score 214.4; DB 9; Length 97083;  
Best Local Similarity 99.5%; Pred. No. 1.2e-41;  
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;



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BASE COUNT      38442 a 35209 c 34033 g 42235 t 1701 others
ORIGIN

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Best Local Similarity 99.5%; Pred. No. 1.3e-41;
Matches 215; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 71535 GGAAGCCGACCTGGCGAGAGTAGGGAAGGCGGCTCCGCCGGTGGCTGCT 71476
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QY 75 atcgcttcgagaactactcagcgacgctggaagagtgagggaagtgctgtct 134
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Db 71475 ATCGCTTCGACGAACCTACTCAGCGACGACCTGAGAAAGTTGAGGGAAGTGTCTG 71416
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QY 135 ctgggtctgcagacgcatgtgtaacgtgcagccgaaataaacatgccttcgtct 194
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Db 71415 CTGGGTCTGCACACCGCATGATGATACGTGCACCGAATAAATCAATCCCTTCTGCT 71356
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QY 195 tcagtgtaaaagccacgtgaagatgctgcggtctg 230
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Db 71355 TCAGTGTGAAGGCCACGTCGAGATGCTCGCGCTGG 71320
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RESULT 12
AC010542      188460 bp      DNA      linear      PRI 31-JUL-2001
LOCUS      Homo sapiens chromosome 16 clone RP11-403P17, complete sequence.
DEFINITION      AC010542
ACCESSION      AC010542.7      GI:15042796
VERSION      HTG.
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 188460)
AUTHORS      DOE Joint Genome Institute and Stanford Human Genome Center.
TITLE      Direct Submission
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 188460)
AUTHORS      DOE Joint Genome Institute.
TITLE      Direct Submission
JOURNAL      Submitted (15-SEP-1999) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
3 (bases 1 to 188460)
DOE Joint Genome Institute and Stanford Human Genome Center.
Submitted (31-JUL-2001) DOE Joint Genome Institute, 2800 Mitchell
Drive, Walnut Creek, CA 94598, USA
COMMENT      On Jul 31, 2001 this sequence version replaced gi:13786333.
Draft Sequence Produced by DOE Joint Genome Institute

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www.jgi.doe.gov
finishing completed at Stanford Human Genome Center
www.shgc.stanford.edu
Quality: Phrap Quality >=40 99.5% of Sequence;
Estimated Total Number of Errors is 0.5.
SYS Content:
WT-11780 G23805
WT-11439 G23701
WT-15863 G24307
SHGC-36487 G30204
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WT-13905 G22316.
Location/Qualifiers
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BASE COUNT      53445 a 45434 c 44402 g 45179 t
ORIGIN

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QY 75 atcgcttcgagaactactcagcgacgctggaagagtgagggaagtgctgtct 134
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Db 74623 ATCGCTTCGACGAACCTACTCAGCGACGACCTGAGAAAGTTGAGGGAAGTGTCTG 74682
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QY 135 ctgggtctgcagacgcatgtgtaacgtgcagccgaaataaacatgccttcgtct 194
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Db 74683 CTGGGTCTGCACACCGCATGATGATACGTGCACCGAATAAATCAATCCCTTCTGCT 74742
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QY 195 tcagtgtaaaagccacgtgaagatgctgcggtctg 230
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RESULT 13
AX330610/C      207 bp      DNA      linear      PAT 09-JAN-2002
LOCUS      Sequence 1119 from Patent WO0194629.
DEFINITION      AX330610
ACCESSION      AX330610
VERSION      AX330610.1      GI:18103588
KEYWORDS
SOURCE      human.
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (sites)
AUTHORS      Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
Horrigan,S., Soppet,D.R. and Weaver,Z.
TITLE      Cancer gene determination and therapeutic screening using signature
gene sets
JOURNAL      Patent: WO 0194629-A 1119 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source      1..207
/organism="Homo sapiens"
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BASE COUNT      70 a 43 c 39 g 54 t 1 others
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Query Match      38.4%; Score 205; DB 6; Length 207;
Best Local Similarity 99.5%; Pred. No. 7.3e-40;
Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 303 caacattgacagtggtgagaggggtgttgcactgtgtacagcagtatgctgtccg 362  
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 Db 207 CAACATTGACAGTTGTTGGAGGGGTTGTGACTTGTACAGCAGATATGCTTCTTGCCG 148  
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 QY 363 acggggcccttattaccgggaagcttctgttcaatccacagcggtccctaccagaaaagc 422  
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 Db 147 ACGGGGCCCTTATTATCCGGAGAGCTTCTGTCAATCCACGCGGTCTTACAGNAAAAGC 88  
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 QY 423 ctgtgcatagaanaaaagaagtttgttaatttatacttctttagttgataactagt 482  
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 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTGATTAAGT 28  
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 QY 483 ataaacataattctgtattcttcca 508  
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 Db 27 ATTAACATATTCTGTATTCTTCCA 2  
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RESULT 14  
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 LOCUS AX330787 207 bp DNA linear PAT 09-JAN-2002  
 DEFINITION Sequence 1296 from Patent WO0194629.  
 ACCESSION AX330787  
 VERSION AX330787.1 GI:18103765  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (sites)  
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
 Horrigan, S., Soppet, D.R. and Weaver, Z.  
 Cancer gene determination and therapeutic screening using signature  
 gene sets  
 Patent: WO 0194629-A 1296 13-DEC-2001;  
 Avalon Pharmaceuticals (US)  
 FEATURES  
 source 1. 207  
 Location/Qualifiers  
 /organism="Homo sapiens"  
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 BASE COUNT 70 a 43 c 39 g 54 t 1 others  
 ORIGIN

Query Match 38.4%; Score 205; DB 6; Length 207;  
 Best Local Similarity 99.5%; Pred. No. 7.3e-40;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 303 caacattgacagtggtgagaggggtgttgcactgtgtacagcagtatgctgtccg 362  
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 QY 363 acggggcccttattaccgggaagcttctgttcaatccacagcggtccctaccagaaaagc 422  
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 Db 147 ACGGGGCCCTTATTATCCGGAGAGCTTCTGTCAATCCACGCGGTCTTACAGNAAAAGC 88  
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 QY 423 ctgtgcatagaanaaaagaagtttgttaatttatacttctttagttgataactagt 482  
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 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTGATTAAGT 28  
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 QY 483 ataaacataattctgtattcttcca 508  
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 Db 27 ATTAACATATTCTGTATTCTTCCA 2  
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RESULT 15  
 AX331008/C  
 LOCUS AX331008 207 bp DNA linear PAT 09-JAN-2002  
 DEFINITION Sequence 1517 from Patent WO0194629.  
 ACCESSION AX331008  
 VERSION AX331008.1 GI:18121642  
 KEYWORDS  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE  
 1 (sites)  
 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,  
 Horrigan, S., Soppet, D.R. and Weaver, Z.  
 Cancer gene determination and therapeutic screening using signature  
 gene sets  
 Patent: WO 0194629-A 1517 13-DEC-2001;  
 Avalon Pharmaceuticals (US)  
 FEATURES  
 source 1. 207  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 BASE COUNT 70 a 43 c 39 g 54 t 1 others  
 ORIGIN

Query Match 38.4%; Score 205; DB 6; Length 207;  
 Best Local Similarity 99.5%; Pred. No. 7.3e-40;  
 Matches 205; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 303 caacattgacagtggtgagaggggtgttgcactgtgtacagcagtatgctgtccg 362  
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 Db 207 CAACATTGACAGTTGTTGGAGGGGTTGTGACTTGTACAGCAGATATGCTTCTTGCCG 148  
 |||||||  
 QY 363 acggggcccttattaccgggaagcttctgttcaatccacagcggtccctaccagaaaagc 422  
 |||||||  
 Db 147 ACGGGGCCCTTATTATCCGGAGAGCTTCTGTCAATCCACGCGGTCTTACAGNAAAAGC 88  
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 QY 423 ctgtgcatagaanaaaagaagtttgttaatttatacttctttagttgataactagt 482  
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 Db 87 CTGTGCATGAAAAAAGAGTTTGTATTTATTTACTTTTGTGATTAAGT 28  
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 QY 483 ataaacataattctgtattcttcca 508  
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 Db 27 ATTAACATATTCTGTATTCTTCCA 2  
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Search completed: July 17, 2002, 09:19:58  
 Job time: 11688 sec







Page 3

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    41 aserValaleulelproglunhrthrhleutrvallglyly 57
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617 TCOCCTTGTG..... 627
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        ::::|||:::: ::|||::::|
628 ..... AGCATTGTGACTGTACTAGTTCATGCA..... 657
    74 uleryarqlysleueuhphasProsergclYprotryghlnylsySp 91
        ||||||| ::|
658 .....AGGAAGCTGTgtgcccat.....TACAGACAATCACG 688
    91 roVALHtSGILySLYS 96
        ||::::::|
689 GAAAGCACACAAAAGAAG 705

seq_name: /cgcn2_6/prodata/2/inna/_5A_COMB.seq:US-08-061-092A-2

seq_documentation_block:
? Sequence 2, Application US/08061092A
? Patent No. 5587458
? GENERAL INFORMATION:
? APPLICANT: KING, C R
? APPLICANT: KASPRZYK, Philip G
? APPLICANT: BIRD, Robert E
? TITLE OF INVENTION: ANTI-edrb-2 ANTIBODIES, COMBINATIONS
? TITLE OF INVENTION: THEREOF, AND THERAPEUTIC AND DIAGNOSTIC USES THEREOF
? NUMBER OF SEQUENCES: 11
? CORRESPONDENCE ADDRESS:
? ADDRESSER: Burns, Doane, Swecker & Mathis
? STREET: George Mason Bldg., Washington & Prince Sts.
? CITY: Alexandria
? STATE: Virginia
? COUNTRY: United States
? ZIP: 22313-1404
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/M5-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/061,092A
? FILING DATE: 14-MAY-1993
? CLASSIFICATION: 424
? ATTORNEY/AGENT INFORMATION:
? NAME: Meuth, Donna M
? REGISTRATION NUMBER: 36, 607
? REFERENCE/DOCKET NUMBER: 018797-014
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 836-6620
? TELEFAX: (703) 836-2021
? INFORMATION FOR SEQ ID NO: 2:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 720 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: double
? TOPOLOGY: linear
? MOLECULE TYPE: DNA (genomic)
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 1..720
? ;
? -08-061-092A-2

alignment_scores:      Length: 72
Quality:       66.50   Gaps:
Ratio:         1.583
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Percent Similarity: 58.333 Percent Identity: 30.556

# alignment\_block:

US-09-801-115-2 x US-08-061-092A-2/rev ..

Align seg 1/1 to reverse of: US-08-061-092A-2 from: 1 to: 720

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28 llelleasnsrleuvalthrThValPheMetLeuIleValSerValle 44
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
604 GTAGTACTATACATAGTATAGCACTATAGTATATAGCAAGCAAGTAT 635
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
44 u.....AlaleuIleProGluThrThrLeuThrValGly.... 56
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
634 AGACGGCAGGTCTCTCAGATGTCAGGCTGCTGAGCTGAGTGAAGTGGCCG 585
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
57 ..GlyGlyValAlPheAlaLeuValThrAlaValCysCysLeuAlaAspGly 72
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
584 TTGGAGGA.....TGTGTCTGCTGTTTACTGTCCTT 553
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
73 AlaleuIleTyArgLys.....LeuLeuPheAsnPr 83
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
552 GCCCTGGAATTGCGGTCAATACAGTATACCATTCATCAGATGATGATCC 503
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
83 osergIyProTyArgL 88
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
502 ATCCATTCATTCAG 487

```

seq\_name: /cgn2\_6/ptodata/2/1na/5A\_COMB.seq:US-09-356-952-12

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seq_documentation_block:
; Sequence 12, Application US/09356952
; Patent No. 6117663
; GENERAL INFORMATION:
; APPLICANT: Boriack-Sjodin, Ann
; APPLICANT: Margalit, S. M.
; APPLICANT: Bor-Sogal, Dafna
; APPLICANT: Cole, Philip
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: A CRYSTAL OF A RAS-SOS COMPLEX AND METHODS OF USE
; FILE REFERENCE: 600-1-228M
; CURRENT APPLICATION NUMBER: US/09/356,952
; EARLIER FILING DATE: 1999-07-19
; EARLIER APPLICATION NUMBER: 60/093,631
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 43676
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
; US-09-356-952-12

```

## alignment\_scores:

| Quality:                   | Ratio:                   | Length: |
|----------------------------|--------------------------|---------|
| 65.50                      | 1.523                    | 78      |
| Percent Similarity: 55.128 | Percent Identity: 33.333 | Gaps: 3 |

## alignment\_block:

US-09-801-115-2 x US-09-356-952-12/rev ..

Align seg 1/1 to reverse of: US-09-356-952-12 from: 1 to: 43676

```

33 ValThrThrPheMetLeuIleValSerValleAlaLeuIleProG 49
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
43598 GTCCGTAAGCGTTGCTTGTATCGTTAGTCACTCTCACTATTTC 43549
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
49 urhrthrThrLeuThrValGly.....GlyGly 59
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
43548 TACACAAATATATGAAGTAAATGATGATTCGCAATTCGTCGATGGC 43499
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
59 alPheAlaLeuValThrAlaValCysCysLeuAlaAspGlyAlaLeu 75

```

43498 TTTACGGCGCTTTTACCTTATATCTGCTTGTATGACATCGAATATCT 43449

76 TyArgLysLeu...LeuPheAsnProSerGlyProTyArgLysLysPr 91  
 43448 TATATAGCGCTAAGTGTGGCTGACCCACTATATACGAATATATAAAC 43399

91 o.....ValHisGluLysLysGluValLeu 99  
 43398 ATCAGTTAAGCTTTCTACCAAGACGACGACTCTG 43365

seq\_name: /cgn2\_6/ptodata/2/1na/5A\_COMB.seq:US-08-684-862-9

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seq_documentation_block:
; Sequence 9, Application US/08684862
; Patent No. 5759541
; GENERAL INFORMATION:
; APPLICANT: Bach, Alfred
; APPLICANT: Hillen, Heinz
; APPLICANT: Bialojan, Siegfried
; TITLE OF INVENTION: No. 5759541el Proteins, the Preparation and Use
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
; COMPUTER: IBM AT-compatible, 80286 processor
; OPERATING SYSTEM: MS-DOS version 5.0
; SOFTWARE: Wordperfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,862
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/361,705
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/966,040
; FILING DATE: 30-DEC-1992
; APPLICATION NUMBER: PCT/EP91/01361
; FILING DATE: 19-JUL-1991
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1333 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; ORIGINAL SOURCE:
; ORGANISM: Agkistrodon rhodostoma
; FEATURE:
; LOCATION: 231 to 935
; OTHER INFORMATION: the coding region shown in (2)(ix)(b)
; US-08-684-862-9

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## alignment\_scores:

| Quality:                   | Ratio:                   | Length: |
|----------------------------|--------------------------|---------|
| 64.50                      | 2.150                    | 56      |
| Percent Similarity: 53.571 | Percent Identity: 33.929 | Gaps: 2 |

## alignment\_block:

US-09-801-115-2 x US-08-684-862-9/rev ..

Align seg 1/1 to reverse of: US-08-684-862-9 from: 1 to: 1333

Thu Jul 18 17:22:02 2002

us-09-801-115-2.rml

Page 5

```
39 leu1eValserValleuAlaLeu1leProgluThrThrLeuThrVa 55
|||||:|||||:|||||:|||||:|||||:
1295 CTTATTATTCTTCTCTCGATTCCTGACATTTCTACAGTCATTT 1246
55 lGlyGlyAlaAlaLeuValThraAlaValCysCysLeuAlaAsp 72
|||||:|||||:|||||:|||||:|||||:
1245 TATCCAACTGTTTCTTCTGCTCCGATTTAGTTGCTTAAGGAT 1197
72 lYAlaLeu1leThrArgLysLeuLeuPheAsnProSerGlyProTyrla 88
|||||:|||||:|||||:|||||:|||||:
1196 .....AAGTTGTTTCTCCAACTTCTGATTTTC... 1167
89 LysLysProValHisGlu 94
|||||:|||||:
1166 .....CCCCCCCCAAG 1155

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-462-844-1

seq_documentation_block:
; Sequence 1, Application US/09462844
; Patent No. 6258563
; GENERAL INFORMATION:
; APPLICANT: Quax, Wilhelmus J.
; TITLE OF INVENTION: Increasing Production of Proteins in
; FILE REFERENCE: GC385-US
; CURRENT APPLICATION NUMBER: US/09/462,844
; PRIOR FILING DATE: 1998-07-15
; PRIOR APPLICATION NUMBER: EP 97305286.3
; PRIOR FILING DATE: 1997-07-16
; PRIOR APPLICATION NUMBER: EP 97305344.0
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Bacillus subtilis
; US-09-462-844-1

alignment_scores:
Quality: 64.50 Length: 91
Ratio: 1.402 Gaps: 3
Percent Similarity: 50.549 Percent Identity: 28.571

alignment_block:
US-09-801-115-2 x US-09-462-844-1 ..
Align seg 1/1 to: US-09-462-844-1 from: 1 to: 2211
16 SerVallyslGlyHisValysMelleuArgLeuAspIleIleAsnSerle 32
|||||:|||||:|||||:|||||:|||||:
1132 TCCTGTAAGGCTTTCGACATGCTGATTCGATTTTCGACAGCTT 1181
32 uValThrThrValPheMetLeu1leValSerValleuAlaLeu1leProG 49
|||||:|||||:|||||:|||||:|||||:
1182 TATCCCTCCGCTTTC...TATCGAGATTTCTCTGCTCTCTGCTG 1228
49 luthThrThrLeuThrValAlGlyGlyAlaPheAlaLeuValThraAla 65
|||||:|||||:|||||:|||||:
1229 AAGAGAGATGCTGATTCGGAAGAAAGCTGCTTTCG... 1266
66 ValCysCysLeuAlaAspGlyAlaLeu1leThrArgLysLeuLeuPheAs 82
|||||:|||||:|||||:|||||:
1267 .....GTCATTAAGAAACATATCATGCA 1289
82 n.....ProserGlyProTyrlGlu 90
|||||:|||||:|||||:
1290 TATTGAGATACGATGAAATACAGAGCCGATACGCCATTCACAAAT 1339
```

```
90 yspProValHisGlyLysGlu 97
|||||:|||||:
1340 GGGATTTCAGACAGCAAAACCCAA 1362

seq_name: /cgn2_6/ptodata/2/lna/6A_COMB.seq:US-08-772-270A-14

seq_documentation_block:
; Sequence 14, Application US/08772270A
; Patent No. 6019984
; GENERAL INFORMATION:
; APPLICANT: MacInnes, Janet
; APPLICANT: Ricciatti, Paul
; APPLICANT: Mallard, Bonnie
; APPLICANT: Rosendal, Soren
; TITLE OF INVENTION: NOVEL BACTERIAL PREPARATIONS, METHOD FOR
; TITLE OF INVENTION: PRODUCING SAME, AND THEIR USE AS VACCINES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bereskin & Parr
; STREET: 40 King Street West
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5H 3J2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/772,270A
; FILING DATE: December 23, 1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Gravelle, Micheline
; REGISTRATION NUMBER: 40,261
; REFERENCE/DOCKET NUMBER: 6580-81
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 364-7311
; TELEFAX: (416) 361-1398
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7721 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Actinobacillus pleuropneumoniae
; US-08-772-270A-14

alignment_scores:
Quality: 64.50 Length: 101
Ratio: 1.240 Gaps: 4
Percent Similarity: 51.485 Percent Identity: 22.772

alignment_block:
US-08-801-115-2 x US-08-772-270A-14/rev ..
Align seg 1/1 to reverse of: US-08-772-270A-14 from: 1 to: 7721
22 LysMelleuArgLeuAspIleIleAsnSer..... 31
|||||:|||||:|||||:|||||:
7519 CCTCTCTTAGACTTTCAGTATAGATTTCTTAATGAGTACTGACTAGCA 7470
32 leuValThrThrValPheMetLeu1leValSerValleuAlaLeu1leP 48
|||||:|||||:|||||:|||||:
7469 ACTGATACACGCTGCTCTCTGTTTAAATTCGCAATACGCTCATTC 7420
48 rogluthrThr.....ThrleuThrValGlyGlyAlaPheAlaLeu 62
|||||:|||||:|||||:|||||:
7419 CAGAACCTAATGATTTCTTATACCACTGTTAAAGTTTCTTGTTA 7370
```

63

ValThrAlaVal.....CysCysLeuAl 70

7369 ATCTCAATATAGATTAATAAACAAGCTGAGGGTGTCTCAATAGC 7320

70 AAspOlyAlaLeuIleTyrArg..... 77

7319 ATCAAGAGTAAATAGTACTTTTCCATGAGATTAACCATATCTGTGT 7270

78 .....LysLeuLeuPheAsnProSerGlyProTyrGlnLys 90

7269 AGGAAAGTTTCCACTTAAATACCTGCTGTCATTTCAACAAA 7220

91 Pro 91

7219 CCA 7217

seq\_name: /cgn2\_6/ptodata/2/ina/6B\_COMB.seq:US-08-976-259-70

seq\_documentation\_block:

Sequence 70, Application US/08976259

Patent No. 6316609

GENERAL INFORMATION:

APPLICANT: Dillon, Patrick J.

APPLICANT: Choi, G.H.

APPLICANT: Welch, Rodney A.

TITLE OF INVENTION: Nucleotide Sequence of Escherichia coli

Patent No. 6316609

NUMBER OF SEQUENCES: 142

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein &amp; Fox P.L.L.C.

STREET: 1100 New York Ave, N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage

OPERATING SYSTEM: HP Vectra 486/33

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/976,259

FILING DATE: Herewith

CLASSIFICATION: 536

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/031,626 AND US 60/061,953

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488, 0740002/EKS/CBM

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 70:

SEQUENCE CHARACTERISTICS:

LENGTH: 17710 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-08-976-259-70

alignment\_scores:

Quality: 64.00

Ratio: 1.231

Percent Similarity: 52.000

Percent Identity: 25.000

alignment\_block:

US-09-801-115-2 x US-08-976-259-70

Align seg 1/1 to: US-08-976-259-70 from: 1 to: 17710

ORIGINAL SOURCE:  
ORGANISM: PAG1069RP  
US-08-998-416-176

alignment\_scores:  
Quality: 63.50 Length: 109  
Ratio: 1.351 Gaps: 5  
Percent Similarity: 43.119 Percent Identity: 25.688

alignment\_block:  
US-09-801-115-2 x US-08-998-416-176 ..

Align seg 1/1 to: US-08-998-416-176 from: 1 to: 654

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28 1lelleasnerleuvalThrThrValaPheMetleuIleValSerValle 44
   ::::: :::::|||||::: ||::: ||::: ||:::
127 CTCGTGCTGCGCATGTCATGTCACGAGCTGCGCCCTCGTCTG 176
   44 uAlaLeuIle.....ProGluThrThrLeuThrValGlyGly.... 57
   ||| :::: ||:::|||||::: ||::: ||::: ||:::
177 TGTGCTGTGGGTATGCCGACGCGGCCCTCACACGCGCGCGCAC 226
   58 ..GlyValPheAlaLeuValThr.....AlaValCysCysLeuAlaasp 71
   |||:::|||| ||::: ||::: ||::: ||::: ||:::
227 TTGGGGCCTTTCACATGCTCCAGCGTGAGCGCTGTGATGCTGCG 276
   72 .....GlyAlaLeuIleTyr..... 76
   |||:::|||||::: ||::: ||::: ||::: ||:::
277 CTCCTCTCCGCCATTAAGTCGAGAGCTGTATCTATGCTACTCAAGCT 326
   76 ..... 76
   CGCGGTATAGCCTTGTATATATATACTTACGCTGCGAGCGCCATATCCGGA 376
   327
   77 .....ArgLysLeuLeuPheAsnProSer 84
   377 CACAGCTATATATTGGCCGCGCTCTCCGCGCTGCTGGGAGCGCAGT 426
   85 GlyProTyrGlnLysLysProValHis 93
   427 GACCCACACCCGATGATGCGCTTGAC 453

```

seq\_name: /cgn2\_6/plodata/2/lna/5B\_COMB.seq:US-09-377-155-8

seq\_documentation\_block:

```

; Sequence 8, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; US-09-377-155-8

```

alignment\_scores:

Quality: 63.50 Length: 77  
Ratio: 1.512 Gaps: 3  
Percent Similarity: 54.545 Percent Identity: 36.364

alignment\_block:

US-09-801-115-2 x US-09-377-155-8/rev ..

Align seg 1/1 to reverse of: US-09-377-155-8 from: 1 to: 1785

```

11 ArgProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAs 27
   ::::: ||::: ||::: ||::: ||::: ||::: ||:::
926 AAGCCTTCGCTTGTCTGTAGAAATCATCTCCGCTTGTCTTAC 877
   27 pileleAsn.....SerleuValThrThrValPheMet...L 39
   ::::: ||::: ||::: ||::: ||::: ||::: ||:::
876 AGTACCAACTTACCGCTTCTTCTTGTATACAGAACTCTTCGACCGA 827
   39 euIleValSerValLeuAlaLeuIleProGluThrThrThrLeuThrVal 55
   ::::: ||::: ||::: ||::: ||::: ||::: ||:::
826 TTTAACCTTGGCTTCTCTGCGGCTTGTCTTGTCCATATACAGTGC 777
   56 GlyGlyGlyValPheAlaLeuValThrAlaValCysCysLeuAlaaspG 72
   ||| ||::: ||::: ||::: ||::: ||::: ||:::
776 GTTGTCTTGTATCTGCGCTCAGACATCGACTGTGTGAATGTCGGAC 727
   72 LysAlaLeuIleTyrArgLysLeuPhe 81
   |||:::|||||::: ||::: ||::: ||::: ||::: ||:::
726 GAATCAACGTTATCGGAAGCTGTTGAC 698

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seq\_name: /cgn2\_6/plodata/2/lna/5B\_COMB.seq:US-09-669-974-8

seq\_documentation\_block:

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; Sequence 8, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Neisseria meningitidis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1782)
; US-09-669-974-8

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alignment\_scores:

Quality: 63.50 Length: 77  
Ratio: 1.512 Gaps: 3  
Percent Similarity: 54.545 Percent Identity: 36.364

alignment\_block:

US-09-801-115-2 x US-09-669-974-8/rev ..

Align seg 1/1 to reverse of: US-09-669-974-8 from: 1 to: 1785

```

11 ArgProPheCysPheSerValLysGlyHisValLysMetLeuArgLeuAs 27
   ::::: ||::: ||::: ||::: ||::: ||::: ||:::
926 AAGCCTTCGCTTGTCTGTAGAAATCATCTCCGCTTGTCTTAC 877

```

```

27 pilelleasn.....SerleuValThrThrValPheMet...L 39
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
876 AGTAAACCACTTACCGCTCTTTCTTGATACAGAGCTTTCGCCACCGA 827
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
39 euileValSerValleuAlaLeuAlaLeuProGluThrThrThrLeuThrVal 55
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
826 TTTTAACCTGCGTCTCTGCGCTCTGCTTCTGCTTCCACATTAACAGTGC 777
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
56 GlyGlyGlyValPheAlaLeuVal.ThrAlaValCysCysLeuAlaAspG 72
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
776 GTTGTCTTTCGATCTGCGCTCAAGACTGCTGCTGCTAAGTCGCGAC 727
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
72 LylAlaLeuIleTyrArgLysLeuPhe 81
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
726 GAATCAACGTTATCGAAGCTGTCTTCTAC 698

seq_name: /cgn2_6/ptodata/2/lna/6B_COMB.seq:US-09-367-206-6

seq_documentation_block:
; Sequence 6, Application US/09367206
; Patent No. 6326482
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: NSP Molecules
; FILE REFERENCE: P1223RIE
; CURRENT APPLICATION NUMBER: US/09/367,206
; CURRENT FILING DATE: 1999-08-09
; PRIOR APPLICATION NUMBER: PCT/US99/08847
; PRIOR FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: US 60/082,767
; PRIOR FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: US 60/113,296
; PRIOR FILING DATE: 1998-12-22
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 6
; LENGTH: 2153
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-367-206-6

alignment_scores:
Quality: 63.50 Length: 112
Ratio: 1.095 Gaps: 5
Percent Similarity: 51.786 Percent Identity: 24.107

alignment_block:
US-09-801-115-2 x US-09-367-206-6 ..

Align seg 1/1 to: US-09-367-206-6 from: 1 to: 2153

20 HISVALVSMetleuArgleuAspIlelleAsnSerleuValThrThrVal 36
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1452 CATGGCCGCGACCTAGCCTAGACCTGTGAAAGTTCCACACCATGTC 1501
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
36 lPheMetleuIleValSerValleu..... 44
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1502 CATCATGCTGCGCGTGCATCTCTGGGCTCACCGGCTCGCGAGAGAGC 1551
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
45 .....AlaLeuIleProGluThrThrThrLeuThrValGly..... 56
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1552 GCGAGCGCTGCTGCACAGACCATTCAGCTGCGCGCGAGACTACGGGG 1601
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
57 .....GlyGlyValPheAlaLeuValThrAlaValCysCysLeu..... 69
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1602 ACTATGGCGACATGTTCAAGCTTCGCGCGGTGATGGTGCCTGACAT 1651
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
69 ..... 69
1652 GGCTGAGATTCTCGGCTGAGAGACATGGGTGACCTCGGCGAGCGAC 1701
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
70 ..AlaAspIylAlaLeuIleTyrArgLysLeuPheAsnProSergly 85

```

```

1702 ACACAGAGGGTGCATCTCTGACAGAGAAGAGCTC.....AAG 1739
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
86 ProTyrGlnLysLysProValHISglulysLysGlu 97
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
1740 CCTTTTCTCAAGAGC...CTCAAGAGGGCAAGAA 1772
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||

seq_name: /cgn2_6/ptodata/2/lna/5A_COMB.seq:US-08-249-420-1

seq_documentation_block:
; Sequence 1, Application US/08249420
; Patent No. 5484724
; GENERAL INFORMATION:
; APPLICANT: El-Sherbeini, Mohamed
; APPLICANT: Clemas, Joseph
; TITLE OF INVENTION: DNA ENCODING GLS1
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Christine E. Carly
; STREET: 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/249,420
; FILING DATE: 26-MAY-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Carly, Christine E.
; REGISTRATION NUMBER: 36,099
; REFERENCE/DOCKET NUMBER: 19162
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-6734
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1854 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-249-420-1

alignment_scores:
Quality: 63.00 Length: 27
Ratio: 3.150 Gaps: 0
Percent Similarity: 74.074 Percent Identity: 51.852

alignment_block:
US-09-801-115-2 x US-08-249-420-1 ..

Align seg 1/1 to: US-08-249-420-1 from: 1 to: 1854

8 lIelYsHsArgProPheCysPheSerValLysGlyHsValLysMetle 24
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
544 ATTATCCAAAGCAATTTTGTACAAAGTGAAAGGTTGAACTAATATCT 593
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
24 uArgLeuAspIlelleAsnSerleuValThr 34
   :||| :||| :||| :||| :||| :||| :||| :||| :||| :|||
594 TCGCTAGAGCCATGAAATTCATCTGTTACT 624

```

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: July 17, 2002, 06:04:05 ; Search time 1777.03 Seconds  
(without alignments)  
4055.854 Million cell updates/sec

Title: US-09-801-115-1  
Perfect score: 534  
Sequence: 1 gtcccaactcgaagtgaag.....aaaaaaaaaaaaaaaaaaaaa 534

Scoring table: IDENTITY\_NDC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estba:\*  
2: em\_esthm:\*  
3: em\_estin:\*  
4: em\_estmu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hci:\*  
9: g\_d\_estcl:\*  
10: g\_d\_est2:\*  
11: g\_d\_hci:\*  
12: g\_d\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description         |
|------------|-------|-------------|--------|-------|---------------------|
| 1          | 505.8 | 94.7        | 524    | 10    | BG705303 602687808  |
| 2          | 492.4 | 92.2        | 962    | 10    | BG249994 602362062  |
| 3          | 491.8 | 92.1        | 510    | 10    | BF399486 UI-R-CA1-  |
| 4          | 487   | 91.2        | 781    | 10    | BG529072 602579169  |
| 5          | 485.4 | 90.9        | 487    | 10    | BM472086 AGENCOURT  |
| 6          | 482.4 | 90.3        | 534    | 10    | BG031757 602299819  |
| 7          | 468.2 | 87.7        | 529    | 10    | BF691818 602247787  |
| 8          | 468   | 87.6        | 468    | 10    | BF109912 7171f03.x  |
| 9          | 467.6 | 87.6        | 930    | 10    | BF203359 601865968  |
| 10         | 462   | 84.6        | 452    | 9     | AT078580 0237005.x  |
| 11         | 445   | 83.3        | 533    | 9     | AT1743235 w990402.x |
| 12         | 432.4 | 81.0        | 453    | 9     | AV754613 AV754613   |
| 13         | 430.4 | 80.6        | 432    | 9     | AA429945 2w67f10.s  |
| 14         | 427   | 79.0        | 427    | 9     | AA455042 aa04a07.s  |
| 15         | 415.2 | 77.8        | 423    | 9     | AT128804 9a94d08.s  |
| 16         | 413.8 | 77.5        | 443    | 9     | BG613984 602641513  |
| 17         |       |             | 432    | 9     | AV759888 AV759888   |

|    |       |      |     |    |                             |
|----|-------|------|-----|----|-----------------------------|
| 18 | 412.4 | 77.2 | 543 | 10 | BG532587 602562152          |
| 19 | 403   | 75.5 | 815 | 10 | BF215121 601846829          |
| 20 | 402.6 | 75.4 | 409 | 9  | AT826623 wk35d10.x          |
| 21 | 399.4 | 74.8 | 402 | 9  | AT989747 wu21f09.x          |
| 22 | 399   | 74.7 | 399 | 9  | AA516431 ne58a03.s          |
| 23 | 394.4 | 73.9 | 396 | 9  | AM183193 xj67f11.x          |
| 24 | 391   | 73.2 | 391 | 9  | AT1989739 wu21e10.s         |
| 25 | 386   | 72.3 | 386 | 9  | AA911088 ok67e01.s          |
| 26 | 384.4 | 72.0 | 385 | 9  | AA989129 or75h10.s          |
| 27 | 381   | 71.3 | 395 | 9  | AT141284 9a52h10.s          |
| 28 | 374.4 | 70.1 | 468 | 10 | W52820 zc55c06.r1           |
| 29 | 363   | 68.0 | 522 | 10 | W38899 zb32d04.r1           |
| 30 | 361.6 | 67.7 | 389 | 9  | AA305052 EST176055          |
| 31 | 357.6 | 67.0 | 456 | 10 | BE875161 601488641          |
| 32 | 353   | 66.1 | 353 | 9  | AT265924 qx68d08.x          |
| 33 | 349.4 | 65.4 | 692 | 11 | AF151058 Homo sapi          |
| 34 | 337.6 | 63.2 | 409 | 10 | N89912 zb22g09.s1           |
| 35 | 337.2 | 63.1 | 380 | 9  | AA477156 0811a06.s          |
| 36 | 331.4 | 62.1 | 333 | 9  | AA987264 BE737159 601305091 |
| 37 | 329.8 | 61.8 | 789 | 10 | BE737159 601305091          |
| 38 | 327.6 | 61.3 | 381 | 9  | AA644621 a74c11.r           |
| 39 | 326.2 | 61.1 | 331 | 10 | BF388158 UI-R-CA1-          |
| 40 | 324.4 | 60.7 | 326 | 9  | AT263261 qp62b12.x          |
| 41 | 324   | 60.7 | 325 | 9  | AT371387 9084b02.x          |
| 42 | 319.4 | 59.8 | 678 | 10 | BI561562 B561562 603256264  |
| 43 | 319   | 59.7 | 319 | 9  | AT349474 q72f07.x           |
| 44 | 317.6 | 59.5 | 491 | 10 | W19506 zb22g09.r1           |
| 45 | 306   | 57.3 | 332 | 10 | BG940590 ax06e11.f          |

## ALIGNMENTS

RESULT 1  
LOCUS BG705303 524 bp mRNA linear EST 07-MAY-2001  
DEFINITION 602687808F1 NIH-MGC\_95 Homo sapiens CDNA clone IMAGE:4820568 5',  
mRNA sequence.  
ACCESSION BG705303 GI:13979504  
VERSION BG705303.1  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 524)  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.  
CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shliraki  
Toshiyuki and Piero Carninci (RIKEN)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
http://image.llnl.gov  
Plate: L1AM10725 row: 0 column: 01  
High quality sequence stop: 521.  
Location/Qualifiers  
1..524  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4820568"  
/clone\_id="NIH-MGC\_95"  
/tissue\_type="hippocampus"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pBluescriptR (modified  
pBluescript KS+); Site:1: BamHI; Site:2: SalI-xhoI (ctgacg  
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',  
size-selected for average insert size 2.5 kb and

## FEATURES

source

normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carinci, in preparation). Library constructed by M. Brownstein (NIH/NCRI, National Institutes of Health). Note: this is a NIH-MGC Library."

BASE COUNT 142 a 113 c 138 g 131 t  
ORIGIN

Query Match 94.7%; Score 505.8; DB 10; Length 524;  
Best Local Similarity 99.6%; Pred. No. 4.6e-62;  
Matches 507; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 gtgaagccagagctggtgaggaaggaagggcggtctccgcgcggtggtgtgt 74  
D 4 GGGAGGCGGAGCTGGGAGAGTAGGAGGAGGCGGTCTCCGCCGCGGTGTGT 63  
QY 75 atgccttcgagaaaccttaagcagcagcagcagcagcagcagcagcagcag 134  
D 64 ATGCTTCGCGAGAACCTTACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 123  
QY 135 ctgggtctgacagcagcagcagcagcagcagcagcagcagcagcagcagcag 194  
D 124 CTGGGTCTGCGAGAGCGCATGATATACGCGAGCCGAAATTAACATGCGCC 183  
QY 195 tcaagtgtgaagcagcagcagcagcagcagcagcagcagcagcagcagcag 254  
D 184 TCAGTGTGAAGGCGCAGTGAAGATGCTGCGGTGATATTATCACTACAGTGA 243  
QY 255 cagatattcagcagcagcagcagcagcagcagcagcagcagcagcagcag 314  
D 244 CAGTATTACGCTCATGCTGATCTGTGTGCGACATGATACGAAACCAACAT 303  
QY 315 ttgggtgaggggt 374  
D 304 TTGGTGGAGGGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 363  
QY 375 tttaacggaagctctgttcaatcccgagcggtcttaacggaagcgtgtgat 434  
D 364 TTACCGGAGAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 423  
QY 435 aaaaagaatttgaattatattatattatattatattatattatattatatt 494  
D 424 AAAAAAGAGTTTGTATTTATTTATTTATTTATTTATTTATTTATTTATTT 483  
QY 495 tctgttcttcccaaaaaaaaaaaaaa 523  
D 484 TCTGTCTCTCCAAAAA 512

RESULT 2  
LOCUS BG249994 962 bp mRNA 1linear EST 13-FEB-2001  
DEFINITION 602362062P1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:4470662 5',  
mRNA sequence.  
ACCESSION BG249994  
VERSION BG249994.1 GI:12759810  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE 1 (bases 1 to 962)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/ILNL at:  
http://image.llnl.gov  
Plate: LLAM10288 row: k column: 15  
High quality sequence stop: 516.  
Location/Qualifiers

FEATURES  
source

1.962  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4470662"  
/clone\_id="NIH\_MGC\_90"  
/issue\_type="adenocarcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: Liver; Vector: pCMV-Sport6; Site\_1: NotI; Site\_2: SalI; Cloned unidirectionally; Oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH-MGC Library."  
BASE COUNT 334 a 199 c 288 g 141 t  
ORIGIN

Query Match 92.2%; Score 492.4; DB 10; Length 962;  
Best Local Similarity 99.6%; Pred. No. 2.5e-60;  
Matches 504; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 29 ggggagaagtgaaggagggcggtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 88  
D 1 GGGGAGAGTAGGGAGGGGCGGTCTCCGCCGCGGTGCTGTGCTGTGCGAGAA 60  
QY 89 cctactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 148  
D 61 CCTACTCAGCGACGCCAGCTGAGAGAGATTAGGAGAGAGTCTGCTGTGCGAG 120  
QY 149 gcgatgatacgtgtgacgcggaataaataacacatgccttctgtcaagtgtga 208  
D 121 GCGATGAGTACGTCGACGCCGAAATTAACATGCGCCCTTGTGTGCTGTA 180  
QY 209 cagctgaagatgt 268  
D 181 CACGTGAGATGCTGCGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 240  
QY 269 atcgtatctgt 328  
D 241 ATCGTATCTGT 300  
QY 329 ttggaactgtgacagcagcagcagcagcagcagcagcagcagcagcagcagc 388  
D 301 TTGGACCTGTGACAGCATATGCTGTGTGTGTGTGTGTGTGTGTGTGTGT 360  
QY 389 ctgttcaatcccgagcgtctctaccagaaagccgtgtcatgaaaaaagaagttg 448  
D 361 CTGTCATATCCAGCGGCTGCTTACCGAAGAAAGCCGTGTGATGAAAAAGAG- 419  
QY 449 taatttatattatattatattatattatattatattatattatattatatt 508  
D 420 TAATTTTATATTACTTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 479  
QY 509 aaaaaaaaaaaaaaaaaaaaaa 534  
D 480 CAAAAA 505

RESULT 3  
LOCUS BF399486/c 510 bp mRNA 1linear EST 27-NOV-2000  
DEFINITION UT-R-CAL-bjb-b-12-0-UI.s1 UT-R-CAL Rattus norvegicus cDNA clone  
UT-R-CAL-bjb-b-12-0-UI 3', mRNA sequence.  
ACCESSION BF399486  
VERSION BF399486.1 GI:11384494  
KEYWORDS EST.  
SOURCE Norway rat.  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



REFERENCE Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
 AUTHORS Rattus.  
 TITLE 1 (bases 1 to 510)  
 JOURNAL Bonaldo, M.F., Lennon, G. and Soares, M.B.  
 MEDLINE Normalization and subtraction: two approaches to facilitate gene  
 COMMENT discovery  
 genome Res. 6 (9), 791-806 (1996)  
 97044477  
 CONTACT: Soares, MB  
 PROGRAM for Rat Gene Discovery and Mapping  
 UNIVERSITY of Iowa  
 451 Eckstein Medical Research Building Iowa City, IA 52242, USA  
 TEL: 319 335 8250  
 FAX: 319 335 9565  
 Email: msoares@blue.weeg.uiowa.edu  
 The sequence contained an oligo-dT track that was present in the  
 oligonucleotide that was used to prime the synthesis of first  
 strand cDNA and therefore this may represent a bonafide poly A  
 tail. cDNA library preparation: M.B. Soares Lab Clone distribution:  
 clones will be available through Research Genetics (www.resgen.com)  
 Seq primer: M13 Forward  
 POLYA=Yes.

FEATURES  
 SOURCE location/Qualifiers  
 1..510  
 /organism="Rattus norvegicus"  
 /strain="Sprague-Dawley"  
 /db\_xref="taxon:10116"  
 /clone="UI-R-CA1-bjb-b-12-0-UI"  
 /clone\_1db="UI-R-CA1"  
 /lab\_host="DH10B (Life Technologies)"  
 /note="Vector: pMT3D-Pac (Pharmacia) with a modified  
 polylinker. Site\_1: Not I; Site\_2: Eco RI; The UI-R-CA1  
 library is a subtracted library derived from the following  
 tissues: thalamus, cerebellum, hypothalamus, medulla, pons  
 and hippocampus. For a detailed description of the library  
 from which this clone was derived, please visit our web  
 site at [ratseq.eng.uiowa.edu](http://ratseq.eng.uiowa.edu). The subtraction has been  
 previously described in (Bonaldo, Lennon and Soares,  
 Genome Research 6:791-806, 1996)  
 TAG\_SEQ=None found"

BASE COUNT 130 a 131 c 104 g 145 t

ORIGIN

Query Match 92.1%; Score 491.8; DB 10; Length 510;  
 Best Local Similarity 99.6%; Pred. No. 4.3e-60;  
 Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 28 gggcggaagtagggagggggtgctccgagcggtgctgctatcgctcgaga 87  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 495 GGGCGGAAGTAGGGAGGGGGGCTGCTCCGCCGCGGTGGCTATCGCTCGAGA 436  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 88 acctactcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 147  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 435 ACCTACTCAGCGCAGCGAGAGAGAGTGAAGGAAAGTCTGCTGCTCGAGA 376  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 148 cgcgagatgataagtcgagcgcgaataaacaacgccccttcgcttcagttgaaag 207  
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 DB 375 CGCGATGGAATACGTGACGCCGAATAAATCAATCGCCCTTCTGCTTCAGTGAAGG 316  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 208 ccaacgtaaatgctgagctgagatataatcaactcactgttaacaacagtatcatgct 267  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 315 CCACGTAATGATCTGCGGCTGATATTAACAACACTGTAACAACAGATTCATGCT 256  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 268 catcgatctgtgtgctgactgataccagaaacacacacatgtgcaattgtgagaggt 327  
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 DB 255 CATCGTATCTGTGTGGCACATGATACAGAAACCAACATTCAGTGTGAGAGGCT 196  
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 QY 328 gtttgacactgtgacagcagcagcagcagcagcagcagcagcagcagcagcagc 387  
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 DB 195 GTTTCACCTTGTGACAGCAGATGCTGCTTGGCGAGCGGCGCTTATTTACGGAAAGCT 136

QY 388 tctgttaaccgccagcggtccttaccagaaagccctgtgcatataaaaaagaagttt 447  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 135 TCTGTCAATCCAGCGGCTCTTACGAGAAAAACCGCTGTGATGATAAAAAAGAGTTT 76  
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 QY 448 gtaattatacttacttttagttgactgaactgaactgaactgaactgaactgaact 507  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 75 GTATTTTATTTACTTTTGTGTTGATTAAGTAAATTAATATTTCTATTTCTTAA 16  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 508 aaaaaaataaaaaa 522  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 15 AAAAAAAAAAAAAA 1  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 4  
 BG529072 781 bp mRNA linear EST 03-APR-2001  
 LOCUS 602579169P1 NIH\_MGC\_60 Homo sapiens cDNA clone IMAGE:4713305 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BG529072  
 VERSION BG529072.1 GI:13520609  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 781)  
 AUTHORS NIH-MGC <http://mhc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: DCTD/drp  
 cDNA Library Preparation: CLONTECH Laboratories, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L10C1556 row: 1 column: 18  
 High quality sequence stop: 475.  
 Location/Qualifiers  
 1..781  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_1db="NIH\_MGC\_60"  
 /tissue\_type="adrenocorticaloma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /note="Organ: prostate; Vector: pDNR-LIB (Clontech);  
 Site\_1: SfiI (ggcgctcgcc); Site\_2: SfiI (ggcattatgac  
 ); Double-stranded cDNA was prepared from cell line RNA.  
 5' and 3' adaptors were used in cloning as follows: 5'  
 adaptor sequence: 5'-ATTCTAGAAGCGGAGGCGGCGGAGCAGTGTG-3'  
 (where B = A, C, or G and N = A, C, G, or T). Average  
 insert size 1.5 kb (range 0.9-4.0 kb). 14/15 colonies  
 contained inserts by PCR. This library was enriched for  
 full-length clones and was constructed by Clontech  
 Laboratories (Palo Alto, CA). Note: this is a NIH\_MGC  
 library."

BASE COUNT 228 a 157 c 233 g 163 t

ORIGIN

Query Match 91.2%; Score 487; DB 10; Length 781;  
 Best Local Similarity 98.7%; Pred. No. 1.6e-59;  
 Matches 512; Conservative 0; Mismatches 5; Indels 2; Gaps 2;

QY 17 gaacccgagcggcgaggaagtagggagggcggtgctccgagcggtgagcgtgctat 76  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 DB 1 GAAGCGGAGCTGGGCGAAGTAGGAGGAGGCGGTGCTCCGCCGCGGTGCTAT 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 QY 77 cgttcgagaaacttaccagcagcagcagcagcagcagcagcagcagcagcagcagc 136

Db 61 CGCTTGGAGAACCTTACCTGAGCAGCCAGCTGAGAGAGTTGAGGGAAGTCTGCTGCT 120  
 QY 137 gggtctgacagcagcgtatgatacgtgcaagccgaaataaataacatcgccctctgcttc 196  
 Db 121 GGGCTGACAGACCGATGATGATACGTGACGCCGAAATTAACATCGCCCTTCTCTTC 180  
 QY 197 agtctgaagcagcagcgtgaagatgctgcgctgataatatacaactcactggttaacaa 256  
 Db 181 AGTGTGAAGCCACAGTGAAGATGCTGGCGGTGGATATTATCACTCATGTGTAACAA 240  
 QY 257 gtatcatgctcactgatactgctgctgctgctgctgatacagaacacacacattgacagt 316  
 Db 241 GTATTCTATGCTCATGATGATGCTGCTGGCTGATGATGATGATGATGATGATGAT 300  
 QY 317 ggtgagaggggtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 376  
 Db 301 GGTGAGAGGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 377 taccggaagcttctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 436  
 Db 361 TACCAGGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
 QY 437 aaagaagcttctgataatctgataatctgataatctgataatctgataatctgataatct 496  
 Db 421 AAGGAGG-TTTTTAATTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 479  
 QY 497 t-gtattcttcaaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 534  
 Db 480 TGGTATCTTCCAG 518

RESULT 5  
 LOCUS BM472086 487 bp mRNA linear EST 05-FEB-2002  
 DEFINITION AGECOURT\_6469731 NIH\_MGC\_92 Homo sapiens cDNA clone IMAGE:5576339  
 5', mRNA sequence.  
 ACCESSION BM472086  
 VERSION BM472086.1 GI:18521128  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 487)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM12328 row: a column: 12  
 High quality sequence stop: 486.  
 Location/Qualifiers  
 1..487  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5576339"  
 /clone\_1db="NIH\_MGC\_92"  
 /tissue\_type="embryonal carcinoma, cell line"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: testis; Vector: PCMV-SPORE6; Site: 1: Not;  
 Site: 2: Sall; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 2.5 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC library."

BASE COUNT

135 a 103 c 121 g 128 t

## ORIGIN

Query Match 90.9%; Score 485.4; DB 10; Length 487;  
 Best Local Similarity 99.8%; Pred. No. 3,4e-59;  
 Matches 486; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 36 agtaagagagagcgtgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 95  
 Db 1 AGTAGGGAGAGGGCGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 60  
 QY 96 aggcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 155  
 Db 61 AGGAGGCGACCTGAG 120  
 QY 156 ataacgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 215  
 Db 121 ATAACTGACAGCGGAAATATAAATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
 QY 216 agatgctgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 275  
 Db 181 AGATGCTGCGGCTGAT 240  
 QY 276 ctgtgtgctgacgtatgatacagcagcagcagcagcagcagcagcagcagcagcagcagc 335  
 Db 241 CTGTGTTGACCTGAT 300  
 QY 336 ctgtgacagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 395  
 Db 301 TTGTGACAGCAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
 QY 396 atccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 455  
 Db 361 ATCCAGCGGCTCTTCCAG 420  
 QY 456 abattacttctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgctgct 515  
 Db 421 ATATTACTTTTATGTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 480  
 QY 516 aaaaaa 522  
 Db 481 AAAAAA 487

RESULT 6  
 LOCUS BG031757 534 bp mRNA linear EST 24-JAN-2001  
 DEFINITION 60229819F1 NIH\_MGC\_87 Homo sapiens cDNA clone IMAGE:4394093 5',  
 mRNA sequence.  
 ACCESSION BG031757  
 VERSION BG031757.1 GI:12422364  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 534)  
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: cgapbs-remail.nih.gov  
 Tissue Procurement: DCTD/DTP  
 CDNA Library Preparation: Life Technologies, Inc.  
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 Cloning Distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: LLM10089 row: e column: 06  
 High quality sequence stop: 446.  
 Location/Qualifiers  
 1..534

FEATURES

1..534





QY 145 agacgcatgataacgtgacgacgcaataataacatccctctctgcttcagtgtga 204  
 DB 121 AGACGCATGATGATACGACGCCGAAATATAACATGCCCCCTCTGCTTACGTGTA 180  
 QY 205 aggcacgtgaagatgctgcgcgtgatataatacaactcgtgtaaacagattatc 264  
 DB 181 AGGCACGTGAAGATGCTGCGCGGTGATATATCAACTGATGTAACAGTATTCAT 240  
 QY 265 gctcatgcatctgtgtgtgacgtataccagaacacacacatgtacgtgtgtgag 324  
 DB 241 GCTCATGATCTGTGTGGCAGTATACAGAAACCAACATTGACAGTTGGTGAAG 300  
 QY 325 ggtgttgacattgtgacagatagtctgtctgcacagcgccctattaccgga 384  
 DB 301 GGTG-TTCACACTTGACAGAGATGCTGCTTCCGACGGGGCCCTTATTTACGGAA 359  
 QY 385 gctcctgtcaatccacagcgctcctaccagaanaagcctgtgtgtgtgtgtgt 444  
 DB 360 GCTTCTGTCAATCCACAGCGGTCTTACAGAAAGCCTGTGATGAAAGAAAGAG- 418  
 QY 445 ttgttaattatattacttttagttgatactaatgttaacatattctgtattc 504  
 DB 419 TTTGTAATTTATATATTACTTTTAA-TTGATATCTAAGTATTAACTATTCTGTATCT 477  
 QY 505 tccaaaaaataaaaaaataaaaaa 534  
 DB 478 TCACAAAAAATAAACAAAAA 507

RESULT 10 452 bp mRNA linear EST 10-AUG-1998  
 AI078580/c LOCUS  
 DEFINITION 0237h05.x1 Soares\_NHMPu\_S1 Homo sapiens cDNA clone IMAGE:1677561  
 3', mRNA sequence.  
 ACCESSION AI078580  
 VERSION AI078580.1 GI:3412988  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 452)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Journal Gene Index  
 COMMENT Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Seq primer: -40m13 fwd. ET from AmerSham  
 High quality sequence stop: 410.  
 Location/Qualifiers  
 1..452  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:1677561"  
 /clone\_lib="Soares\_NHMPu\_S1"  
 /tissue\_type="pooled human melanocyte, fetal heart, and  
 pregnant uterus"  
 /lab\_host="DH10B"  
 /note="Organ: mixed (see below); Vector: pT7T3D-Pac  
 (Pharmacia) with a modified polylinker; Site\_1: Not I;  
 Site\_2: Eco RI; Equal amounts of plasmid DNA from three  
 normalized libraries (melanocyte 2NbM, pregnant uterus  
 NDHPV, and fetal heart NBH119W) were mixed, and as circles  
 were made in vitro. Following HAP purification, this DNA  
 was used as tracer in a subtractive hybridization  
 reaction. The driver was PCR-amplified cDNAs from pools of  
 5,000 clones made from the same 3 libraries. The pools  
 consisted of I.M.A.G.E. clones 260232-265223,  
 340488-345479, and 484488-489479."

BASE COUNT

125 a 110 c 97 g 120 t

## ORIGIN

Query Match 84.6%; Score 452; DB 9; Length 452;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-54;  
 Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 cgcggtgctgtgtctatcgtcttcgacgaactactcagcagcagcgtggaagtgtg 118  
 DB 452 CGCGGTGCGGTTGCTTTCGTTGCGAAGACCTACTGACGCGCAGCTGAGAAAGTTG 393  
 QY 119 agggaaagtgctgt 178  
 DB 392 AGGAAAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 333  
 QY 179 catgccctctctctcagtgatgaagacagcagcagcagcagcagcagcagcagc 238  
 DB 332 CATGCCCT 273  
 QY 239 aactcactgtgaacacagatattcatgtcatcgtatctgtgtgtgtgtgtgtgtgt 298  
 DB 272 AACTCAGTGTGATACAGAGTATTCATGCTCATGCTATGCTGTGTGCACTGATACG 213  
 QY 299 accacaacattgacagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 358  
 DB 212 ACCACAACATTGACAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 153  
 QY 359 gccgagcgcccttattaccggaagctctgttcaatccacagcgctcctaccagaa 418  
 DB 152 GCCGAGCGGCGCTTATTTACCGGAAGCTTCTGTTCAATCCACGCGCTTACCGA 93  
 QY 419 aagcctgtcatgaanaaagaagtttgaattatattacttttagttgact 478  
 DB 92 AAGCCTGTGATGAAAGAAAGTTTGTATTTATATTACTTTTGTGTTACT 33  
 QY 479 aagatttaacattttctgtattcttccaa 510  
 DB 32 AAGTATTAACTATTCTGTATCTTCCAA 1

RESULT 11 453 bp mRNA linear EST 20-DEC-1999  
 AI743235/c LOCUS  
 DEFINITION wg90a02.x1 Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1 Homo sapiens cDNA clone  
 IMAGE:2372330 3', mRNA sequence.  
 ACCESSION AI743235  
 VERSION AI743235.1 GI:5111523  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 453)  
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Journal Gene Index  
 COMMENT Unpublished (1997)  
 CONTACT: Robert Strausberg, Ph.D.  
 EMAIL: cgapbs-r@mail.nih.gov  
 This clone is available royalty-free through LNL; contact the  
 IMAGE Consortium (info@image.lnl.gov) for further information.  
 Insert Length: 378 Std Error: 0.00  
 Seq primer: 40UP from Gibco.  
 Location/Qualifiers  
 1..453  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:2372330"  
 /clone\_lib="Soares\_NSF\_F8\_9W\_OT\_PA\_P\_S1"  
 /lab\_host="DH10B"  
 /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with  
 a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
 Equal amounts of plasmid DNA from five normalized

1450092-145335, 1477220-148103, 148872-149255, 15002 -  
150407, 151176-152327 Soares NB21F8-9w pool 1:  
758280-760583, 772104-774407 Soares NB9PA pool 1:  
304776-306511, 320136-322823, 336280-336663 Soares NB10T  
pool 1: 737320-736407, 739080-740999 Soares NBOR  
Soares and M. Fatima Ronaldo.  
109.5 93.0  
109.5 93.0

|                       |                 |                    |           |             |
|-----------------------|-----------------|--------------------|-----------|-------------|
| Query Match           | 83.3%           | Score 445;         | DB 9;     | Length 453; |
| Best Local Similarity | 98.9%           | Pred. No. 1.6e-53; |           |             |
| Matches 448;          | Conservative 0; | Mismatches 5;      | Indels 0; | Gaps 0;     |

[illegible]

DY 121 ggaaagtgtctgtctggtctctgcagacgcgatgataacgtgcagccgaaaataaacca 180

QY 181 tcgcccctctgtcagtgtagaaagccacgtgaagatgtctgcgctqatattatcaa 240

QY 241 ctcaactgtaacaacagtatctcatgctcatcgtatctgtttgqcactqaataccagaanaac 300

QY 301 cacaacattgacagttgtgtggaqqqtqtttqcacttqtqacaqcaqatatactatctta 360

361 cgacgqgqccctatttaccgqaaacttctattcaatcccaacgatccttaccgaagaaaaa 120

421 qccttqcatgaaaaaaqaattttqtaattttatatattactttttanttttataactaa 480

OY 481 qtattaaacattttctctatattcttccaaaaaa 513

AV754613  
LOCUS  
AV754613  
533 bp  
mpvux 11444444  
ccm 10 ccm 0000

|           |            |             |
|-----------|------------|-------------|
| ACCESSION | AV754613   |             |
| VERSION   | AV754613 1 | CT:10913461 |

| ORGANISM | Homo sapiens | Fukariyota, Volvox, Chlamydomonas reinhardtii |
|----------|--------------|---|
|          |              |   |

REFERENCE  
AUTHORS  
1 (bases 1 to 533)  
Song H, Dong Y, Gu Y, Wang W, Qian M, et al. (2014) The genome of the Chinese hamster ovary cell line V79. *Genomics* 104: 101–107.

W., Tu, Y., Jia, J., Fu, G., Ren, S., Zhong, M., Lu, G., Hu, R., Ye, M., Zhang, Q.

JOURNAL  
COMMENT  
Unpublished (2000)  
Contact: Orlan Sh...

contact: yinghua zhang

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/organism="Homo sapiens"  
/db xref="taxon:9606"
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/clone_lib="tp"  
/tissue_type="pituitary tumor"
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/note="Vector: pTriplex2; Site_1: sflIA; Site_2: s
BASE COUNT      149      113      145      130      4

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| Match | Local Similarity | Pred. No. | Conservative | Matches |
|-------|------------------|-----------|--------------|---------|
| 487   | 95.58            | 8.7e-52   | 0            | 13      |
| 488   | 95.58            | 8.7e-52   | 0            | 13      |
| 489   | 95.58            | 8.7e-52   | 0            | 13      |
| 490   | 95.58            | 8.7e-52   | 0            | 13      |
| 491   | 95.58            | 8.7e-52   | 0            | 13      |
| 492   | 95.58            | 8.7e-52   | 0            | 13      |
| 493   | 95.58            | 8.7e-52   | 0            | 13      |
| 494   | 95.58            | 8.7e-52   | 0            | 13      |
| 495   | 95.58            | 8.7e-52   | 0            | 13      |
| 496   | 95.58            | 8.7e-52   | 0            | 13      |
| 497   | 95.58            | 8.7e-52   | 0            | 13      |
| 498   | 95.58            | 8.7e-52   | 0            | 13      |
| 499   | 95.58            | 8.7e-52   | 0            | 13      |
| 500   | 95.58            | 8.7e-52   | 0            | 13      |

Dbb  
35 ACCGCAACCGCAGCTCCGCCGCCTTGGATTCGTCTTTT

[illegible][illegible][illegible][illegible][illegible]

caaccacggaagcaccgllccaaaccagcggcccttaaccagaaaaagcctgtgcata

QY 433 aaaaagaagtttltgtaatttataattactttttaqtttqatactaagtaataaacata 4

22 5' - G A A T T T A T A T T A C T T T T T A G T T T G A T A C C T A A G T A T T A A C A T A 3'

204 111CIGIAITICTITACAAAAA 533

RESOL 13  
AA429945/C

| DEFINITION         | zwb/110.s1 soares_testis_NHT | Homo sapiens | CDNA clone | IMAGE:7 |
|--------------------|------------------------------|--------------|------------|---------|
| 3' / mRNA sequence |                              |              |            |         |

VERSION AA429945.1 GL:2113244  
KEYWORDS EST.

**SOURCE** human.

| REFERENCE                 | ORGANISM   | Authors   |
|---------------------------|--|---|
| 1 (bases 1 to 432)        | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. | Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schellenberg, K., Steptoe, M., Tan, F., Theisling, B., White, Y., Wyllie, T., Waterston, R. and Wilson, R. |
| TITLE                     | Washington University School of Medicine   |   |
| JOURNAL                   | 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  |   |
| COMMENT                   | Tel: 314 286 1800  |   |
|                           | Fax: 314 286 1810  |   |
|                           | Email: estewartson.wustl.edu   |   |
|                           | This clone is available royalty-free through LLNT ; contact the  |   |
|                           | IMAGE Consortium (info@image.llnl.gov) for further information.  |   |
|                           | Seq primer: -4n1m3 fwd. EF from Amer sham  |   |
|                           | High quality sequence stop: 421.   |   |
| FEATURES                  | Location/Qualifiers  |   |
| SOURCE                    | 1..432   |   |
|                           | /organism="Homo sapiens"   |   |
|                           | /db_xref="taxon:9606"  |   |
|                           | /clone="IMAGE:781291"  |   |
|                           | /clone_1id="Soares_testis_NHT"   |   |
|                           | /sex="male"  |   |
|                           | /lab_host="DH10B"  |   |
|                           | /note="Vector: pT73D-Pac (Pharmacia) with a modified   |   |
|                           | polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA   |   |
|                           | was prepared from mRNA obtained from Clontech Laboratories   |   |
|                           | , Inc., and primed with a Not I - Oligo(dt) primer [5',  |   |
|                           | TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTT 3'].   |   |
|                           | Double-stranded cDNA was ligated to Eco RI adaptors  |   |
|                           | (Pharmacia), digested with Not I and cloned into the Not I   |   |
|                           | and Eco RI sites of the modified pT73 vector. Library  |   |
|                           | went through one round of normalization to Cot5, and was   |   |
|                           | constructed by Bento Soares and M. Fatima Bonaldo. "   |   |
| BASE COUNT                | 119 a  |   |
| ORIGIN                    | 101 c  |   |
|                           | 92 g   |   |
|                           | 120 t  |   |
| Query Match               | 80.6%; Score 430.4; DB 9; Length 432;  |   |
| Best Local Similarity     | 99.8%; Pred. MO. 1.9e-51;  |   |
| Matches 431; Conservative | 0; Mismatches 1; Indels 0; Gaps 0;   |   |
| 81                        | tcgcagaacctactcagcgccagcctgtgaagaagttgaggaagtgctgctgctggt  | 140   |
| 432                       | tcgcagacacctactcagcgccagcctgtgaagaagttgaggaagtgctgctgctggt   | 373   |
| 141                       | cttcgacagcgatcggataacgtgcagccgaaataaacaatcgccctctgcttcagt  | 200   |
| 372                       | cttcgacagcgatcggataacgtgcagccgaaataaacaatcgccctctgcttcagt  | 313   |
| 201                       | tgaagaagccagcgtgaagatcgtcgcgctgtgatatattcaactactactggtataacagat  | 260   |
| 312                       | tgaagaagccagcgtgaagatcgtcgcgctgtgatatattcaactactactggtataacagat  | 253   |
| 261                       | tcattgctcatcgtatctggtgtggaactgtataccagaagaacacaactgacagttggtg  | 320   |
| 252                       | tcattgctcatcgtatctggtgtggaactgtataccagaagaacacaactgacagttggtg  | 193   |
| 321                       | gaagggatgtttgacgtgtgacagcagatagcgtcttggcgcagcgagcgccctattacc   | 380   |
| 192                       | gaagggatgtttgacgtgtgacagcagatagcgtcttggcgcagcgagcgccctattacc   | 133   |
| 381                       | ggaagcctctgttcaatcccgacggtcctctaccagaanaaacctgtgtgcatgaaanaaag   | 440   |
| 132                       | ggaagcctctgttcaatcccgacggtcctctaccagaanaaacctgtgtgcatgaaanaaag   | 73  |
| 441                       | aagtttgtaatttatattactttttagtttgaattctaagtataatacatattctgta   | 500   |
| 72                        | aaattttgtaatttttatattactttttagtttgaattctaagtataatacatattctgta  | 13  |

| QY                        | 501        | ttcttcacaaa  | 512             |                                      |
|---------------------------|------------|--|-----------------|--------------------------------------|
|                           |            |  |                 |                                      |
| Db                        | 12         | TTCTTCACAAA  | 1               |                                      |
| RESULT                    | 14         | AA455042   | 427 bp          | mRNA                                 |
| LOCUS                     | AA455042/c | aa04a07.s1   | Scares_NHMPU_S1 | Homo sapiens cDNA clone IMAGE:812244 |
| DEFINITION                |            | 3', mRNA sequence.   |                 |                                      |
| ACCESSION                 |            | AA455042   |                 |                                      |
| VERSION                   |            | AA455042.1   | GI:2177818      |                                      |
| KEYWORDS                  |            | EST.   |                 |                                      |
| SOURCE                    |            | human.   |                 |                                      |
| ORGANISM                  |            | Homo sapiens   |                 |                                      |
| REFERENCE                 |            | Dukerjola; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  |                 |                                      |
| AUTHORS                   |            | 1 (bases 1 to 427)   |                 |                                      |
|                           |            | Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,D., Moore,B., Schellenberg,K., Stepcue,M., Tan,F., Theisling,B., White,Y., Wyllie,T., Waterston,R., and Wilson,R.  |                 |                                      |
| TITLE                     |            | WashU-Merck EST Project 1997   |                 |                                      |
| JOURNAL                   |            | Unpublished (1997)   |                 |                                      |
| COMMENT                   |            | Contact: Wilson RK<br>Washington University School of Medicine<br>4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108<br>Tel: 314 286 1800<br>Fax: 314 286 1810<br>Email: est@watson.wustl.edu<br>This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.<br>Seq primer: -41m3 fwd. ER from Amer sham<br>High quality sequence stop: 393.<br>Location/Qualifiers<br>1..427  |                 |                                      |
| FEATURES                  |            |  |                 |                                      |
| SOURCE                    |            |  |                 |                                      |
|                           |            | /organism="Homo sapiens"   |                 |                                      |
|                           |            | /db_xref="GDB:6043155"   |                 |                                      |
|                           |            | /db_xref="taxon:9606"  |                 |                                      |
|                           |            | /clone="IMAGE:812244"  |                 |                                      |
|                           |            | /clone_lib="Scares_NHMPU_S1"   |                 |                                      |
|                           |            | /tissue_type="Pooled human melanocyte, fetal heart, and pregnant uterus"   |                 |                                      |
|                           |            | /lab_host="DH10B"  |                 |                                      |
|                           |            | /note="Organ: mixed (see below); Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site:1: Not I; Site-2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NBHPU, and fetal heart NBH119W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479." |                 |                                      |
| BASE COUNT                |            | 119 a  | 101 c           | 116 t                                |
| ORIGIN                    |            |  |                 |                                      |
| Query Match               |            | 80.0%; Score 427; DB 9; Length 427;  |                 |                                      |
| Best Local Similarity     |            | 100.0%; Pred. No. 5,6e-51;   |                 |                                      |
| Matches 427; Conservative |            | 0; Mismatches  | 0; Indels       | 0; Gaps                              |
| QY                        | 81         | tcgcagaacctaccacgcagcagcagctgagagaggttgagggaagtgcctgctgagt   | 140             |                                      |
| Db                        | 427        | TCGCAGAACTACTCAAGCGACCCAGCTTGAGAGAGTTGAGGAAAGTGTCTGCTGGGT  | 368             |                                      |
| QY                        | 141        | ctgcagacgcgagatggataacgctgcagcgcgaaaataaacaatcgccctctgcttcagtg   | 200             |                                      |
| Db                        | 367        | CTGCAGACGCAGTATGATTAACGTGCAGCGCGAAATATTAACAATTCGCCCTTCTGCTTCAAGTG  | 308             |                                      |
| QY                        | 201        | tgaagagccacggtgaagatgctgcgctgtagatattatcaactcaactcgtgtgaacaacaglat   | 260             |                                      |

